

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 31, 2001, 16:29:53 ; Search time 31.09 Seconds

(without alignments)
3187.406 Million cell updates/sec

Title: US-09-250-083a-2

Perfect score: 3942
Sequence: 1 MSFIDPYQHIIIVEHQYSHKF.....LSNVEARFFPKKEFLSKPKKA 749

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_unclassified:*
14: sp_vertebrate:*
15: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3738.5	94.8	748	6	O9TT38
2	2964	75.2	563	4	O9U1Y6
3	732	18.6	1012	4	O9U1Y6
4	732	18.6	1012	4	O9U1Y6
5	499.5	12.7	541	4	O75457
6	494.5	12.5	541	4	O9U655
7	259	6.6	637	3	O9P8P2
8	256.5	6.5	634	3	O9P8L1
9	228.5	5.8	626	3	O42790
10	225.5	5.7	626	3	O42791
11	223	5.7	608	3	O93795
12	216.5	5.5	640	3	O59863
13	209.5	5.3	754	3	O94046
14	209.5	5.3	754	3	O9U1Y6
15	207.5	5.3	605	3	O74207
16	207.5	5.3	605	3	O9U6F6
17	199	5.0	49	4	O14064
18	194.5	4.9	633	3	O917N6
19	192.5	4.9	624	3	O13857

20	178.5	4.5	574	10	O9FY55	O9FY55 arabidopsis
21	172.5	4.4	510	10	O9LEX1	O9LEX1 arabidopsis
22	171.5	4.4	493	10	P92940	P92940 arabidopsis
23	170.5	4.3	613	3	P78854	P78854 schizosach
24	169	4.3	644	3	O9U6H5	O9U6H5 schizosach
25	163.5	4.1	673	3	O9P327	O9P327 schizosach
26	153	3.9	528	10	O9ZVY8	O9ZVY8 arabidopsis
27	144	3.7	583	10	O9FYD9	O9FYD9 arabidopsis
28	140.5	3.6	972	10	O9M2D4	O9M2D4 arabidopsis
29	140.5	3.6	2178	2	O46149	O46149 clostridium
30	138.5	3.5	773	10	O9M2R0	O9M2R0 arabidopsis
31	135.5	3.4	505	10	O48645	O48645 lycopersico
32	129	3.3	1278	8	O36586	O36586 neospora
33	128	3.2	1096	11	O62688	O62688 rattus norv
34	126.5	3.2	2104	3	O42730	O42730 schizosach
35	126.5	3.2	2104	3	O14157	O14157 schizosach
36	126	3.2	694	4	O9Y2J0	O9Y2J0 homo sapien
37	125	3.2	2874	14	O9ODE2	O9ODE2 cyphonectr
38	124.5	3.2	2048	4	O9HBU3	O9HBU3 homo sapien
39	124.5	3.2	2061	4	O9NZM1	O9NZM1 homo sapien
40	124	3.1	2874	14	O9ODE1	O9ODE1 cyphonectr
41	122.5	3.1	1178	3	O12527	O12527 saccharomyc
42	122	3.1	987	5	O9V7I8	O9V7I8 drosophila
43	121.5	3.1	769	10	O9LXU2	O9LXU2 arabidopsis
44	121	3.1	675	10	O65279	O65279 arabidopsis
45	119	3.0	857	10	O9Y0C8	O9Y0C8 arabidopsis

ALIGNMENTS

RESULT 1
O9TT38 PRELIMINARY; PRT; 748 AA.
ID O9TT38;
AC O9TT38;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PHOSPHATIDYL CHOLINE 2-ACYLHYDROLASE CPLA2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
OX [1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=HEART;
RA Al-Khalili O.K., Eaton D.C.;
RT Molecular cloning of cDNA coding for phospholipase A2.*;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF204923; AAF15299.1; -
DR HSSP; P47712; IBCI.
DR InterPro; IPR000008; -
DR InterPro; IPR000209; -
DR InterPro; IPR001596; -
DR InterPro; IPR002642; -
DR Pfam; PF00168; C2; 1.
DR Pfam; PF01735; PLA2_B; 1.
DR PROSITE; PSS0004; C2 DOMAIN 2; 1.
DR PROSITE; PSS00387; PPASE; UNKNOWN_1.
DR PROSITE; PSS00136; SUBSTITLASE_ASP; UNKNOWN_1.
DR SMART; SM00239; C2; 1.
KW Hydrolase.
SQ SEQUENCE 748 AA; 85234 MW; 7661A3EFC41FF668 CRC64;

Query Match 94.8%; Score 3738.5; DB 6; Length 748;
Best Local Similarity 94.3%; Pred. No. 1.3e-279;
Matches 706; Conservative 26; Mismatches 16; Indels 1; Gaps 1;
OY 1 MSFIDPYQHIIIVEHQYSHKFTVVLRATKYTKGAFGMDLPDPYVELFISTPPDSRRRT 60
DB 1 MSFIDPYQHIIIVEHQYSHKFTVVLRATKYTKGAFGMDLPDPYVELFISTPPDSRRRT 60

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QY 61 RHFNNDINFWNNEFEFLIDPNOENVLEITLMDANYVMDETIGATFTVYSMKVGEKKEV 120
DB 61 RHFNNDINFWNNEFEFLIDPNOENVLEITLMDANYVMDETIGATFTVYSMKVGEKKEV 120
QY 121 PRTFNQVTEVMELEMSLEVSCDPLRFSALCDQEKTFROOKREHIESKMLLGPNNSG 180
DB 121 PRTFNQVTEVMELEMSLEVSCDPLRFSALCDQEKAFROOKREHIEENNRKRLGPKKSSG 180
QY 181 LHSARDVPVVALISGGGFRAMVFGSGVMAKALYESGILDCATYVAGLSGSTMVSLYSH 240
DB 181 LKSTRVVPVVALISGGGFRAMVFGSGVMAKALYESGILDCATYVAGLSGSTMVSLYSH 240
QY 241 PDPEPEKPEINEELMKVNSHNPDLTLPQKRYVESLMKKSSGQVPTFTDIFGMLIG 300
DB 241 PDPEPEKPEINEELMKVNSHNPDLTLPQKRYVESLMKKSSGQVPTFTDIFGMLIG 300
QY 301 ETLIHRMHTTSLSEKESVSAQCPLETCVHVPVSELMAFADWVEFSPEIGMAKYG 360
DB 301 ETLIHRMHTTSLSEKESVSAQCPLETCVHVPVSELMAFADWVEFSPEIGMAKYG 360
QY 361 TMAPDLESGKFFMGTVYKKEENPLHFLMGVMSAFSLFRVYLGVSOSRSGTMEEE 420
DB 361 TMAPDLESGKFFMGTVYKKEENPLHFLMGVMSAFSLFRVYLGVSOSRSGTMEEE 420
QY 421 LENTTKHIVNDSDESHEPKGTENEDAGSDYQSDNQASWIRHIMALVSDALFN 480
DB 421 LENTTKHIVNDSDESHEPKGTENEDAGSDYQSDNQASWIRHIMALVSDALFN 480
QY 481 TREGRGKXHNMLGINTSYPLSPDFATQDSFDDDELDAVAADPEFERIYEPDLV 540
DB 481 TREGRGKXHNMLGINTSYPLSPDFATQDSFDDDELDAVAADPEFERIYEPDLV 540
QY 541 KKKKIHVDSGLTFNLPYLIRPQGVDLISFDSARPSDSSPEFKLLAEKAKANN 600
DB 540 KKKKIHVDSGLTFNLPYLIRPQGVDLISFDSARPSDSSPEFKLLAEKAKANN 599
QY 601 KLPPEKIDYVDRGLKCYVFKKPNDEKDCPTIHFVLANINFRKYKAPGVRETE 660
DB 600 KLPPEKIDYVDRGLKCYVFKKPNDEKDCPTIHFVLANINFRKYKAPGVRETE 659
QY 661 EKEETADPFIQDDPSPSTFNQVNOAFKRLHDLMHNTLNINDIVIEKAVESIEYRR 720
DB 660 EKEETADPFIQDDPSPSTFNQVNOAFKRLHDLMHNTLNINDIVIEKAVESIEYRR 719
QY 721 QNPSRCSVLSNVEARFENKEFLSKPKA 749
DB 720 QNPSRCSVLSNVEARFENKEFLSKPKA 748

RESULT 2
Q0UIY6
AC 09UIY6: PRELIMINARY: PRT: 563 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DJ661GJ2.1 (PHOSPHOLIPASE A2, GROUP IVA (CYTOSOLIC, CALCICUM-DEPENDENT) (CP1A2-ALPHA)) (FRAGMENT).
DE GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Frankland J.;
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049797; CAB56229.1; -
DR InterPro; IPR000209; -
DR InterPro; IPR002542; -
DR Pfam; PF01735; PUA2_B.1;
DR ProSite; PS00387; PPASE; UNKNOWN.1.

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DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN.1.
DR SMART; SM00022; PUA2.1.
FR NON_TER
SQ SEQUENCE 563 AA: 63712 MW: DBA3A12DD0467C94 CRC64:

Query Match
Best local similarity 99.8%; Pred. No. 4, 4e-220;
Matches 562; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 187 VPPVAILSGGGFRAMVFGSGVMAKALYESGILDCATYVAGLSGSTMVSLYSHDPEPK 246
DB 1 VPPVAILSGGGFRAMVFGSGVMAKALYESGILDCATYVAGLSGSTMVSLYSHDPEPK 60
QY 247 GPEEINEELMKVNSHNPDLTLPQKRYVESLMKKSSGQVPTFTDIFGMLIGETLIHN 306
DB 61 GPEEINEELMKVNSHNPDLTLPQKRYVESLMKKSSGQVPTFTDIFGMLIGETLIHN 120
QY 307 RMTTSLSEKESVNTAQCPLETCVHVPVSELMAFADWVEFSPEIGMAKYGTFMAD 366
DB 121 RMTTSLSEKESVNTAQCPLETCVHVPVSELMAFADWVEFSPEIGMAKYGTFMAD 180
QY 367 LFGSKFFMGTVYKKEENPLHFLMGVMSAFSLFRVYLGVSOSRSGTMEELENTT 426
DB 181 LFGSKFFMGTVYKKEENPLHFLMGVMSAFSLFRVYLGVSOSRSGTMEELENTT 240
QY 427 KHIIVNDSDESHEPKGTENEDAGSDYQSDNQASWIRHIMALVSDALFNREGRA 486
DB 241 KHIIVNDSDESHEPKGTENEDAGSDYQSDNQASWIRHIMALVSDALFNREGRA 300
QY 487 GKVHNMGLINTSYPLSPDFATQDSFDDDELDAVAADPEFERIYEPDLVSKKIH 546
DB 301 GKVHNMGLINTSYPLSPDFATQDSFDDDELDAVAADPEFERIYEPDLVSKKIH 360
QY 547 VVDSGLTFNLPYLIRPQGVDLISFDSARPSDSSPEFKLLAEKAKANNLPPEK 606
DB 361 VVDSGLTFNLPYLIRPQGVDLISFDSARPSDSSPEFKLLAEKAKANNLPPEK 420
QY 607 IDPYVDRGLKCYVFKKPNDEKDCPTIHFVLANINFRKYKAPGVRETEEKEIA 666
DB 421 IDPYVDRGLKCYVFKKPNDEKDCPTIHFVLANINFRKYKAPGVRETEEKEIA 480
QY 667 DEDIEDPSPSTFNQVNOAFKRLHDLMHNTLNINDIVIEKAVESIEYRONPSRC 726
DB 481 DEDIEDPSPSTFNQVNOAFKRLHDLMHNTLNINDIVIEKAVESIEYRONPSRC 540
QY 727 SVLSNVEARFENKEFLSKPKA 749
DB 541 SVLSNVEARFENKEFLSKPKA 563

RESULT 3
Q05712
AC 095712: PRELIMINARY: PRT: 1012 AA.
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CYTOSOLIC PHOSPHOLIPASE A2 BETA.
DE GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99185108; PubMed-10085124;
RA Pickard R.T., Stiffler B.A., Kramer R.M., Sharp J.D.;
RT "Molecular cloning of two new human paralogs of 85-kDa cytosolic
RL phospholipase A2."
DR EMBL; AF065215; AAC78836.1; -
DR InterPro; IPR000008; -

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DR InterPro: IPRO002642; -.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF01735; PLA2_B; 1.
DR PROSITE: PS00004; C2_DOMAIN_2; 1.
DR SMART: SM00022; PLAC; 1.
SQ SEQUENCE 1012 AA; 114120 MW; 989EDBAD3ACF19DD CRC64

Query Match	18.6%;	Score 732;	DB 4;	Length 1012;
Best Local Similarity	24.9%;	Pred. NO. 1.5e-47;		
Matches 209;	Conservative 152;	Mismatches 267;	Indels 210;	Gaps 26;

QY	21	TVVVLLRRTKTYKGAFGMLTDPDYVLEFSTPDSKRRHFNNDINPWNNEFEEILD	80
Db	244	TVRLQAHRLPS---KOLVPRSDCYVYLMLEPTACSHLQIRTYKWNSSPWNOSFHRIRH	3000
QY	81	PNQENVLEITLMDANYM-DETIGTATFVSMKVG-----KKEVPF--	1222
Db	301	ROLNVMELKVFQDDLVLTGDDPVLSVLFDAAGTLRAGEFRRRESFSLSPQEGGRULEVEFRLQ	3600
QY	123	---IFNOV-----TEMVL-----	132
Db	361	SLADRGEMVLVNSGVARELSCHLVOLEETGDOKSSEHRVOLVVGSGEGPOEASVGTG	420
QY	133	-----EMSLFVSCPD-----	143
Db	421	FREHCPRACMEDELSTRQADAPFEEDLAKPLSALBPGOVYRVLPFSQEPMLRVELKKAAGL	4800
QY	144	---LRFSMALCDOEKTFPQROKKEHIESMKKLLGPKNSEGLSARBPVVALIGSGGF	199
Db	481	RELAVRLGFGPCABEQAFLSRRKQVAAALRAL--QDGDQJDEBIDIPVVALMATGGI	537
QY	200	RAMVGFSGVAKALYESGLIDCAITYAGLSGSTWMTSLYLSHPDEPK--GPEFINELM	236
Db	538	RAMSLYGOAGLAKLELIDLCVSYTASGSTWALMLIYEDPEWSOKDLGAPTEL--LK	594
QY	257	KVNSHNPULLLTPOKRYAYESLKKKSSGOVPYFTQIFGMLGETLIHARMNT--TLSTL	315
Db	595	TQVTKKLGVLAPSOLODRYRQELERARLIGPSCFTMLMA-LINEALLBHPDHKLSIQ	653
QY	316	KEKYNFACQPLPFTCLHVK-PDVSELMFADWVFESEYELGMAKYGTGFMADLFGSKFFM	374
Db	654	REALSHGQNPPLPYCALNTKGQSLTFTEFEGWCEFSYEVGPRYGAFTISELGSSEFM	713
QY	375	GTVVKKTEENDLHFLMGCWGSASFILFNRYLVGSGOSRGSSTMEEL-----ENITTKH	428
Db	714	GOLMKRLPRESRICPLEGSIWMLYA-----ANLQDSLYMASSEPSQFMDRW	757
QY	429	IYVSDSSDSD-----EHEPRGTENEDAGSDYOSDONQASWHRHIMALYDSALFNRREG	484
Db	758	VRNANLADKEDVPLKKEEPRSTVGRIA--EFTFD-----LITWRP	766
QY	485	RAGRYVNFMLGLANTSYPLSPLSDPATODSFDDDELDAVADPEFERIYERLPDYSKK	544
Db	797	LAQTHNFMRLGRLHNRKDYFQHR--HESTWKAITYLDGL-----LTSEPH	841
QY	545	IHVVDGLTFNLPYLLRPQGVYLLISFEDSARPSDSSPFKEKLLIAEKMAKMKLP	604
Db	842	LCILDVAGLYINTSCLPRLQPTRDVLLISLDYNLHGA-----FQQLDGLRFGCEQGIPE	896
QY	605	PKIDPYVFDREGLKECYVEK-PKRNPMDEKQCPITIIHVLNINFRKAKAGVPRETEEK	666
Db	897	PRIPSPDEQOPRECHTFSDPTCP--GAPALVHPLVSDSFRFYSAGV--RRPEEA	951
QY	664	EIAPFDJFDDDESPFSFNFQPYQNAQFKRLHDLHFNFTLNNIDVIRKAMYESIEYRQ	721
Db	952	AAGEVNL--SSDSYHTTKTYTYSOEDVDKLLHLTHYVNCNNQDOLLEALQAOVARRQ	1008
RESULT	4		
090UKV7			
ID	09UKV7	PRELIMINARY;	PRT; 1012 AA.
AC	09UKV7;		

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2001 (TREMBLrel. 16, Last annotation update)
 DE CYTOSOLIC PHOSPHOLIPASE A2 BETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP
 RX MEDLINE=9928796; PubMed=10358058;
 RA Song C., Chang X.-J., Bean K.M., Proia M.S., Knopf J.L., Kriz R.W.
 JT "Molecular characterization of cytosolic phospholipase A2-beta."
 RT J. Biol. Chem. 274:17063-17067(1999).
 DR EMBL: AF121908; A032135.1; -.
 DR InterPro: IPR000008; -.
 DR DR InterPro: IPR002642; -.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF01735; PLA2_B; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR SMART: SM00239; C2; 1
 SQ SEQUENCE 1012 AA; 114154 MW; 1A9D3269BA57797 CRC64;

Query Match	18.6%;	Score 732;	DB 4;	Length 1012;
Best Local Similarity	24.9%;	Pred. No. 1.5e-47;		
Matches 209;	Conservative 152;	Mismatches 267;	Indels 210;	Gaps 26;

QY	21	TVVVVLRATKVKGAFGMLTDPDYVELEISTPDSKRTRHFNNDINPWNEFEETILD	80
Db	244	TVRLQAHRLPS---KDLVTPSDCYVILMLPTACSHLQTRIVYVNSSPPWNSOFHHRH	3000
QY	81	PNQNVLEITLMDANYM-DETLCTATFVSSMKVG-----KKVP--	1211
Db	301	ROLNMVELKFDODLVLTGDDPVLSVLFDAGTLRACEFRRSFSLSPQEGGRLEVEFRQ	3606
QY	122	---FIPNOV-----TEMV-----	1322
Db	361	SLADRGEMFVNSGVLVARELSCLHVOLEETGGDKSSSHRVOVLVPGSCBGPQEAHSVGT	4200
QY	133	-----EMSLVSCSDP-----	1433
Db	421	FRFHCPCWMEQELSTRLODAPEQLKAPLSALPBGQVVRVLFPTSOEPLMRVELKREAGL	4800
QY	144	----LRSMALCDEKTPFRQQRKHITESMKLLGPKNSBLSHARVPYVVALIGSGGF	1999
Db	481	RELAVRLGFGPQCAEEOAFLSRKKOVYAAALQAL---OLOGDLQEDDIPVVALMATGGI	5377
QY	200	RANVFGSGVMALTEESGILDCATVAVAGSGSTWVSTLYSHHPDERK---GPEEINELM	2566
Db	538	RANVSTVGQLAGLKELDGLDCVSTITGASGSTYMLANDIEPEMSQDLIAGPTLL---LK	5946
QY	257	KNVSHNPLLLTPQKVRKYVESLKKKKSSGQVPTFDIFGMLIGETLLIHNRMNT-TLSSL	3153
Db	595	TQVYRNKLGVLAPSOLORYROELAEARLGRPSCFTMLMA-LINEALIHDEPHHKHKSQ	6533
QY	316	KEKNTAOCPPLTFTCLHYK-POVSELMFADWFESEPELGMATYGFPMADLGSKEFM	3740
Db	654	REALSHGONPLPYTICALMTKQOSTLTTEFGEMCEFSPEYEGVFKYGAFTFSELFGSEFM	7133
QY	375	GTVVKKYEENDLHFLMGVGSASFILFNRYLVGVSOSRGSSTMEEL-----ENITTKH	4288
Db	714	GOLMKRLRPESRICFLLEGIMSLYA-----ANLDLSLYMASSEPQFMDRW	7577
QY	429	IYVSDSSSD-----ESHERRGTENEDAGSDYSDNDQNASWLIHRIMALVSDSALFNTREG	4644
Db	758	VRNANDKRECVPLLKIEEPPSTIGRIA-EFFTD-----LTLWRP	7966
QY	485	RAGKVHNMELANTNYSYPSLSDFAPOOSFODELDAVAADDEFERYTEPLDYVSKK	5444
Db	797	LAQTHNPLRKLHNRHXDYQHR--HETSKATITLDGL-----PNO-----LTPSEPH	8411
QY	545	IHAVDSGLTFNLPYPLLRQGVDLIISPEFSARPSDSPPKEILLAEKAMKMKLPF	6040

Db 842 LCLLDVGLINTSCPLLOPTRDVLDSLIDYNLHGA-----FOOQOLGRCOQEGIF 896
OY 605 PRIDPVDFREGKCYVYK-PKNPDMKDCPTIHFVLANINERKKAQVPRETEEK 663
Db 897 PRISPEEQLOPRECHTSPTPC-----GAPAVLHFLVYSOFREYSAPGV-RRTPEEA 951
OY 664 EIAEDFIDDPESPSTENFOYPOAFAKRLHDMHENTLNINDIVKEAMVESIEYRQ 721
Db 952 AAGEVNL-SSSDSPHYHTKVTSQEDVDKLLHLYHVNCONNQELLEALRQAVRRQ 1008

RESULT 5
ID 075457 PRELIMINARY; PRT; 541 AA.
AC 075457;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RX MEDLINE=98371032; PubMed=9705332;
"A novel calcium-independent phospholipase A2, cPLA2-gamma, that is
RT preylated and contains homology to cPLA2."
RL J. Biol. Chem. 273:21926-21932(1998).
DR EMBL: AF058921; AAC32823.1;
DR InterPro: IPR002642;
DR Pfam: PF01735; PLA2_B.1.
DR SMART: SM00022; PLAC1.1.
SQ SEQUENCE 541 AA; 60920 MW; BBB972A611FB5237 CRC64;

Query Match 12.7%; Score 499.5; DB 4; Length 541;
Best Local Similarity 27.0%; Pred. No. 4.5e-30;
Matches 150; Conservative 88; Mismatches 189; Indels 129; Gaps 20;

OY 135 SLEVSCPDRLFSMALCDEKTFROQRKEHIRESMKKLLGPKNSEGLSARDVPVAIIG 194
Db 3 SESEVITIPQLQ-----KEKAVERRRRLHVLKALKL-----RIEADAPVAVAVG 48
OY 195 SGGGFRAVGFSGVWKALYESGILDCATYVAGISGTWMTSLYSHPDPEKPEEINEE 254
Db 49 SGGGLRAHIAACGLVSEMEKEGILDAVYLAGVSGSTWAISSLYTN-----DGDMEALFA 103
OY 255 LKKNVSHNPLLLTPQKVRVYESLKKKSSGQPV-----FTTDIFGMILGETLIH 305
Db 104 DLKH-----RFTROEMDLAKSLQKTIQAARSENYSLTDWMAVWISKOTR 148
OY 306 NRMNTTSLKKEKVTNACPLPLFTCL--HKPVSSELMFAD-WVEFSYEIGMAKYGF 362
Db 149 ELPESHLSMKKRPVEEGTLPRYIFAIDNDLOPSMOEARAPETWEFTPHHAGFALGAF 208
OY 363 MAPDLFGSFFPGTYVKKKEENPLHFLMGVMSAHSIFLNRVLGVSQSRSST----- 416
Db 209 VITTHGSKFKKGRVLRHPRDLTFRLGLWGSAL-----GNTVEYIREY 252
OY 417 MEELLENITTKHI-----VSNDSS-----DSDESHEPKGTENEDAGSDYOD 459
Db 253 IFDOLRLNLTKGLMRAVANAKSIGHLIFARLLRQESSOGHEPP-----EDEG-----GE 304
OY 460 NOASWTHRM-----MALVSDALEFNTREGRAKGVNFMGLNLTSTYPLSLSPATOD 514
Db 305 PHTWLTMLKEMWTRTSLEKQOPHEDPE-RKGSLSNLM-----DEVKKT 348
OY 515 SPDDDELDAVADPDEFER--IYEPIDVSKKIHYVDSGLTFNLPPYLRLRQGVDLII 572

Db 349 GICASKWENGTHNLFYKHGIRDKIMSRKHLHLVDAGLAINTPPVLPPTREVHLIL 408
OY 573 SFDESARPSDPPPEKELLAEKMAKMKLPPPKIDPYFD--REGKCYVFKKPNPM 630
Db 409 SFDFSA-----GDPEFTIATDYCRHKIKTFFQVDEALDLSKAPACIYIKGETG-- 461
OY 631 EKDCPTIHFVLANIN 646
Db 462 ----PVYIHFFLFNID 473

RESULT 6
ID 09UP65 PRELIMINARY; PRT; 541 AA.
AC 09UP65;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CYTOSOLIC PHOSPHOLIPASE A2 GAMMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99185108; PubMed=10085124;
RA Pickard R.T., Striffler B.A., Kramer R.M., Sharp J.D.;
RT "Molecular cloning of two new human paralogs of 85-kDa cytosolic
phospholipase A2."
RL J. Biol. Chem. 274:8823-8831(1999).
DR EMBL: AF065214; AAC78835.1;
DR InterPro: IPR002642;
DR Pfam: PF01735; PLA2_B.1.
DR SMART: SM00022; PLAC1.1.
SQ SEQUENCE 541 AA; 60948 MW; 63E6AE7F7550741 CRC64;

Query Match 12.5%; Score 494.5; DB 4; Length 541;
Best Local Similarity 26.8%; Pred. No. 1.1e-29;
Matches 149; Conservative 88; Mismatches 190; Indels 129; Gaps 20;

OY 135 SLEVSCPDRLFSMALCDEKTFROQRKEHIRESMKKLLGPKNSEGLSARDVPVAIIG 194
Db 3 SESEVITIPQLQ-----KEKAVERRRRLHVLKALKL-----RIEADAPVAVAVG 48
OY 195 SGGGFRAVGFSGVWKALYESGILDCATYVAGISGTWMTSLYSHPDPEKPEEINEE 254
Db 49 SGGGLRAHIAACGLVSEMEKEGILDAVYLAGVSGSTWAISSLYTN-----DGDMEALFA 103
OY 255 LKKNVSHNPLLLTPQKVRVYESLKKKSSGQPV-----FTTDIFGMILGETLIH 305
Db 104 DLKH-----RFTROEMDLAKSLQKTIQAARSENYSLTDWMAVWISKOTR 148
OY 306 NRMNTTSLKKEKVTNACPLPLFTCL--HKPVSSELMFAD-WVEFSYEIGMAKYGF 362
Db 149 ELPESHLSMKKRPVEEGTLPRYIFAIDNDLOPSMOEARAPETWEFTPHHAGFALGAF 208
OY 363 MAPDLFGSFFPGTYVKKKEENPLHFLMGVMSAHSIFLNRVLGVSQSRSST----- 416
Db 209 VITTHGSKFKKGRVLRHPRDLTFRLGLWGSAL-----GNTVEYIREY 252
OY 417 MEELLENITTKHI-----VSNDSS-----DSDESHEPKGTENEDAGSDYOD 459
Db 253 IFDOLRLNLTKGLMRAVANAKSIGHLIFARLLRQESSOGHEPP-----EDEG-----GE 304
OY 460 NOASWTHRM-----MALVSDALEFNTREGRAKGVNFMGLNLTSTYPLSLSPATOD 514
Db 305 PHTWLTMLKEMWTRTSLEKQOPHEDPE-RKGSLSNLM-----DEVKKT 348
OY 515 SPDDDELDAVADPDEFER--IYEPIDVSKKIHYVDSGLTFNLPPYLRLRQGVDLII 572
Db 349 GICASKWENGTHNLFYKHGIRDKIMSRKHLHLVDAGLAINTPPVLPPTREVHLIL 408

QY 573 SFDSARPSDSSPPFKELLAEKMAKNKLPPFKIDPYED--REGLECYVFKPNPDM 630
ID 098P2 PRELIMINARY: PRT: 637 AA.
AC 098P2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE SECRETED PHOSPHOLIPASE B.
GN PLB1.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H99;
RA Cox G.M., McNamee H.C., Gottfredsson M., Chen S.C.A., Wright L.C.,
RT Sorrell T.C., Ghanoun M.A., Perfect J.R.;
RT "Phospholipase B is a virulence factor for Cryptococcus neoformans";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF223383; AAF65220.1; -
DR InterPro: IPR002642; -
DR Pfam: PF01735; PLA2_B.1.
DR SMART: SM00022; PLAC.1.
SQ SEQUENCE 637 AA; 68789 MW; C37B979D69A9330 CRC64;

Query Match 6.6%; Score 259; DB 3; Length 637;
Best Local Similarity 24.1%; Pred. No. 2.1e-11;
Matches 111; Conservative 67; Mismatches 145; Indels 138; Gaps 20;

QY 154 EKFFROQRKHIESKMKLLGPKNSBGLHSARDVPVVAIGSGGGRFAMV-GFSGVYKAL 212
ID 098P2 PRELIMINARY: PRT: 637 AA.
AC 098P2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE SECRETED PHOSPHOLIPASE B.
GN PLB1.
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H99;
RA Cox G.M., McNamee H.C., Gottfredsson M., Chen S.C.A., Wright L.C.,
RT Sorrell T.C., Ghanoun M.A., Perfect J.R.;
RT "Phospholipase B is a virulence factor for Cryptococcus neoformans";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF223383; AAF65220.1; -
DR InterPro: IPR002642; -
DR Pfam: PF01735; PLA2_B.1.
DR SMART: SM00022; PLAC.1.
SQ SEQUENCE 637 AA; 68789 MW; C37B979D69A9330 CRC64;

RESULT 8
ID 098P2 PRELIMINARY: PRT: 634 AA.
AC 098P2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE PHOSPHOLIPASE B.
GN PLB.
OS Filobasidiella neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-3501.
RA Varma A., Kwon-Chung K.J.;
RT "The phospholipase B gene from a serotype D isolate of Cryptococcus
neoformans";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF238241; AAF61964.1; -
DR InterPro: IPR000874; -
DR InterPro: IPR002642; -
DR Pfam: PF01735; PLA2_B.1.
DR PROSITE: PS00257; BOMBESIN; UNKNOWN_1.
DR SMART: SM00022; PLAC.1.
SQ SEQUENCE 634 AA; 68167 MW; E2998B83CFADA925 CRC64;

Query Match 6.5%; Score 256.5; DB 3; Length 634;
Best Local Similarity 23.2%; Pred. No. 3.2e-11;
Matches 107; Conservative 73; Mismatches 139; Indels 143; Gaps 19;

QY 154 EKFFROQRKHIESKMKLLGPKNSBGLHSARDVPVVAIGSGGGRFAMV-GFSGVYKAL 212
ID 098P2 PRELIMINARY: PRT: 634 AA.
AC 098P2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE PHOSPHOLIPASE B.
GN PLB.
OS Filobasidiella neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-3501.
RA Varma A., Kwon-Chung K.J.;
RT "The phospholipase B gene from a serotype D isolate of Cryptococcus
neoformans";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF238241; AAF61964.1; -
DR InterPro: IPR000874; -
DR InterPro: IPR002642; -
DR Pfam: PF01735; PLA2_B.1.
DR PROSITE: PS00257; BOMBESIN; UNKNOWN_1.
DR SMART: SM00022; PLAC.1.
SQ SEQUENCE 634 AA; 68167 MW; E2998B83CFADA925 CRC64;

QY 154 EKFFROQRKHIESKMKLLGPKNSBGLHSARDVPVVAIGSGGGRFAMV-GFSGVYKAL 212
ID 098P2 PRELIMINARY: PRT: 634 AA.
AC 098P2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE PHOSPHOLIPASE B.
GN PLB.
OS Filobasidiella neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales;
OC Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-3501.
RA Varma A., Kwon-Chung K.J.;
RT "The phospholipase B gene from a serotype D isolate of Cryptococcus
neoformans";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF238241; AAF61964.1; -
DR InterPro: IPR000874; -
DR InterPro: IPR002642; -
DR Pfam: PF01735; PLA2_B.1.
DR PROSITE: PS00257; BOMBESIN; UNKNOWN_1.
DR SMART: SM00022; PLAC.1.
SQ SEQUENCE 634 AA; 68167 MW; E2998B83CFADA925 CRC64;

RESULT 9
ID 042790 PRELIMINARY: PRT: 626 AA.
AC 042790;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
 DE LYSPHOSPHOLIPASE.
 GN LPL.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ST. LAWRENCE ST74-OR3-1VA;
 RA Catchside D.E.A., Yeaton P.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF045574; AAC03052.1; -
 DR InterPro; IPR002642; -
 DR Pfam; PF01735; PLA2_B; 1.
 DR SMART; SM00022; PLAC; 1.
 SQ SEQUENCE 626 AA; 67586 MW; 2158D0EDA26E0CDB CRC64;

Query Match 5.8%; Score 228.5; DB 3; Length 626;
 Best local similarity 23.7%; Pred. No. 4.5e-09;
 Matches 117; Conservative 62; Mismatches 155; Indels 159; Gaps 20;

QY 142 PDIFSMALCDEKTFRQQRKHIRESMKLLGPKN-----SEGLHSARDVPVYA 191
 DB 36 PTLRKAVDLSNEKKMNLSTIRKNTTQPMRDLLKRAITGFDETFEENFANNISQLPNYA 95
 QY 192 ILGSGGFRAMVGFSGVMKALYE-----SGILDCATYVAGLSGTWYMTLSYSH 240
 DB 96 IAISSGGYRALMNGAFVAAADNRIONTTGAGIGGLGSLSTYLAGLSGGWLVGSLFSN 155
 QY 241 P-----DFPE---KGPEINEELMKVSHNPILLTPQKRYVE---SLM 280
 DB 156 NFSSTFTLSEKKVDFENSIFKPREAG-----LSYVNRIOYSEVAKAYA 202
 QY 281 KKKSSQPYTFDIFGMLIGETLIHNRN---TTLSSLEKYN--TAOCPLPFTCLHVK 335
 DB 203 KKKDAGFETSTIDYMGRAISYOLIGADMGCPAYTFSSIAOTNFOKAETPFIIVADGRA 262
 QY 336 P-DVSELMFADWVEPSPIGMA---AKYGTFMAPDLFGSKFPMGYVK--KYE--NPLH 387
 DB 263 PGDTTISLNAVYERNEPFTGSMDPVYG-FAPTKYLGANFNGVYIPSGCKVEGLDQAG 321
 QY 388 FLMGVWGAFASTLIFNRVLGVSGSGSGSTMEEBLENTTKHIVSNDSDSDSHPEKGT 447
 DB 322 FVWG-----TSSTLFNGFL-----LANISSYDVARAHNSRDFC--PQGN 360
 QY 448 -ENEDAGSDYQSDNOSWIRHIMALVSDSALFNTREGRAKVHFMGLCLNLTSTPLSP 506
 DB 361 RROEDVDSQIIPNPLDMNRR-----381
 QY 507 LSDFATQDSFDDDELDAVAADPDEFERIVEPLDYKSKTIHVVDGSLTF-NLPYPLLRPQ 565
 DB 382 -----TNPADLTLELD-----LVDDGEDLQNTPLNPLTPQV 412
 QY 566 RGVVDLISDFESA 578
 DB 413 RAVDVIFAVDSSA 425

RESULT 10
 ID 042791 PRELIMINARY; PRT; 626 AA.
 AC 042791;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
 DE LYSPHOSPHOLIPASE.
 GN LPL.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LINDEGREN 25A.
 RA Catchside D.E.A., Yeaton P.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF045575; AAC03053.1; -
 DR InterPro; IPR002642; -
 DR Pfam; PF01735; PLA2_B; 1.
 DR SMART; SM00022; PLAC; 1.
 SQ SEQUENCE 626 AA; 67527 MW; E11B3B059E4E8C2 CRC64;

Query Match 5.7%; Score 225.5; DB 3; Length 626;
 Best local similarity 23.8%; Pred. No. 7.6e-09;
 Matches 118; Conservative 63; Mismatches 151; Indels 163; Gaps 23;

QY 142 PDIFSMALCDEKTFRQQRKHIRESMKLLGPKN-----SEGLHSARDVPVYA 191
 DB 36 PTLRKAVDLSNEKKMNLSTIRKNTTQPMRDLLKRAITGFDETFEENFANNISQLPNYA 95
 QY 192 ILGSGGFRAMVGFSGVMKALYE-----SGILDCATYVAGLSGTWYMTLSYSH 240
 DB 96 IAISSGGYRALMNGAFVAAADNRIONTTGAGIGGLGSLSTYLAGLSGGWLVGSLFSN 155
 QY 241 P-----DFPE---KGPEINEELMKVSHNPILLTPQKRYVE---SLM 280
 DB 156 NFSSTFTLSEKKVDFENSIFKPREAG-----LSYVNRIOYSEVAKAYA 202
 QY 281 KKKSSQPYTFDIFGMLIGETLIHNRN---TTLSSLEKYN--TAOCPLPFTCLHVK 335
 DB 203 KKKDAGFETSTIDYMGRAISYOLIGADMGCPAYTFSSIAOTNFOKAETPFIIVADGRA 262
 QY 336 P-DVSELMFADWVEPSPIGMA---AKYGTFMAPDLFGSKFPMGYVK--KYE--NPLH 387
 DB 263 PGDTTISLNAVYERNEPFTGSMDPVYG-FAPTKYLGANFNGVYIPSGCKVEGLDQAG 321
 QY 388 FLMGVWGAFASTLIFNRVLGVSGSGSGSTMEEBLENTTKHIVSNDSDSDSHPEKGT 447
 DB 322 FVWG-----TSSTLFNGFL-----LANI-----339
 QY 448 ENEDAGSDYQSDNOSWIRHIMALVSDSALFNTREGRAKVHFMGLCLNLTSTPLSP 507
 DB 340 -----SSY--DGVARRAR-----GR-----353
 QY 508 SDPATQ-DSFDDDELDAVAADP--DEFERIVEPLDYKSKTIHVVDGSLTF-NLPYPLLR 563
 DB 354 -DFCQGNRRQEDVDSQIIPNPLDMNRRTPNAD--TLELDVDDGEDLQNTPLNPLTPQ 410
 QY 564 PORGVDLISDFESA 578
 DB 411 PVRAVDVIFAVDSSA 425

RESULT 11
 ID 093795 PRELIMINARY; PRT; 608 AA.
 AC 093795;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
 DE PHOSPHOLIPASE B.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sugiyama Y., Nakashima S., Nozawa Y., Kitajima Y., Mirdod F.;
 RT "Molecular cloning of phospholipase B 2 from Candida albicans.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB010809; BAA36162.1; -
 DR InterPro; IPR002642; -
 DR Pfam; PF01735; PLA2_B; 1.

DR SMART, SM00022, PLAC, 1.
SQ SEQUENCE 608 AA; 67219 MW; 0ABEA2C878CD8610 CRC64;

Query Match 5.7%: Score 223; DB 3; Length 608;
Best Local Similarity 23.1%: Pred. No. 1.1e-08;

Matches 95; Conservative 68; Mismatches 164; Indels 84; Gaps 15;

QY 141 CPDLRFSMALCD---OEKTFROQRKEHRESMKLLGPPKNSGLHSARDY-----187
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 31 CPBGKLRSLSDGINSNEKAYIDRRYANAKSELRF-----LHNAKAVDFVDGFLN 82
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 188 -PYYAILSGGGFRANVGSVAKALYE-----SGLDCAITYAGLSGTWSTL 237
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 83 SNPLIGLAFSGGGYRAMLAGAGELLADSRATNPVSGLIQQSSSYIVLGGSGMLVGL 142
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 238 YSHDPPEKPEEINEMLMNVSHNPLLLTPQVKRYVESLW-----KKSSGQPV 289
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 143 ASDNLLPV--DQLREKRLMDI--ONSLVAYYGVAIVRNT--AMGNINILQVOTKOLAGFTV 198
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 290 TTFDIFGMLIGETLIHRMNTTSLSEKYNVA-----OCPLPLFTCLHVKPPVSELMF 343
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 199 SIDIVYRALSHQLTLPFDNGASFMSDVTETSPQNNEMPRITIALGHEPPTVLMNF 258
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 344 ADWY-EFSPEYIGM--AKYGTMAPDLFGSKFENGTVAKYKYEENPLH--FLMGVWSAF 397
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 259 NSYFELTLPYEVGSMDSLSFVDYTKYIGTRLDGAPVSKRCVGNFAGPFMGCTSSS-- 316
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 398 SILFNRLVYSGSGSRGSTRMEELNTTKHIVS-----NDSDSDDESHEP 444
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 317 -LENTVLQQLNNPIPPFKELISKFTLDEVEKLNIDIAQYNPNPHKSNNSDTKIAQS 374
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 445 KGTENEDAGSDYOSDNOASWIRHIMALVS-----DSALFNTR 483
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 375 RTLYLADGCGEDGQVPLPLIHRKVAIFAEDQADKNNMPDGSALIKTFE 425
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 12
ID 059863 PRELIMINARY; PRT; 640 AA.
AC 059863;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
DE PHOSPHOLIPASE B.
GN KLPB.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 1090.
RA Oishi H., Morimoto T., Watanabe Y., Tamai Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
EMBL: AB014495; BAA28619.1;
DR InterPro: IPR002642;
DR Pfam: PF01735; Pfam2.B: 1.
DR SMART: SM00022; PLAC; 1.
SQ SEQUENCE 640 AA; 69982 MW; 90A696CB5D7FF9E3 CRC64;

Query Match 5.5%: Score 216.5; DB 3; Length 640;
Best Local Similarity 20.2%: Pred. No. 3.9e-08;

Matches 134; Conservative 100; Mismatches 233; Indels 195; Gaps 28;

QY 138 VCSGPD---LRFSMALCDEKTFRQQRKEHRESMKLL-----GPKNS---EGLSHA 184
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 36 VVDCDENINLYRKADAVSDDEADWLKVRHSTVPALDKDFGRKGFINDISIDKLILAT 95
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 185 RD-VPVVAIIAGSGGFRANVGSVAKALYE-----SGLDCAITYAGLSGTWY 233
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 96 QDAPKVAIIACSGGGYRAMLAGAGISAMDRITGDANDHGLIGSLQSYIAGISGGMWL 155
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 234 MSTL-YSHDPPEKPEEINEEL---MKVSNHNPILLPLPQVKRY---VESIMKKSS 285
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 156 VGLLAYNNMTSVQAIINNMTDDNSIMDISNSIVPGGINIFSSISRWDDISDAVEEKKKA 215
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 286 GQPTFTDIDIGMLIG-----ELLHNRMNTLSLK--EKVNTACPLPLTCLHVKRDVS 339
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 216 GFNTSIDVWGRALSYNFFPSLDGGVGYTMTLRDVFKNKGEMPPISVAGRYGTQ 275
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 340 EL-MFADWFESEPEYIEGMAYKGFMAPDLFGSKFPMGTVVKYBENLHFLMGVWSAFS 398
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 276 VVINATVFEENPEPKSMDY-----TLHFTDV-----304
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 399 ILFNRLVGSOSRGSTMEELNTTKHIVSNDSDSDESHEPKGTENEDAGSDYOS 458
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 305 -----RYAGINVTNGTPNVTGKCVAGHDNTG-----330
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 459 DNOASWIRHIMALVSALFNTRREGRAKVNMLGLNLN--TSYPLSLSPATQDSF 516
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 331 -----FVNGTSSSLFN-----OPLQLNTTDLPSFLYNLHGLFTDASD 369
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 517 DDDELAAVADPDEFERIEPLDYKSK-----KIHVDSGLT-FNLPLYLILRPR 566
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 370 DYDDISIMAPNP-----FLEITNIPSNYSOSISEDDTLVYDGGEDCONIPPLQTER 424
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 567 GVDLIISEDESARPSDSSPFKELLAEKNAKM-----NKLPPKI-DPYVFDREGIKEC 620
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 425 EIDVIFALDNSADTDQSWP--DGSLQTYARQGLQKGIAPFYVDVMTGLGNTLR 482
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 621 YVF---KPKN-PDMKDCPTIHFVLNINFRKAKGVPRETEEKELADFIDDPES 676
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 483 PTFEGCDARNLTDESIPPLVYVMPNTRSE-----NS 515
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 677 PESTFENQY-PNOAFKRLHLMHFNLTNID-----VTKEMVSEIEYRQNP 724
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 516 NTFKMSYSTSEKFKMIQNGFEAVTMKLTKDNEMGCISCALIRRKQESLNTTL--PS 573
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 725 RC 726
DB 574 EC 575

RESULT 13
ID 094046 PRELIMINARY; PRT; 754 AA.
AC 094046;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
DE LYSOPHOSPHOLIPASE.
GN CA41C10.12.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1161.
RA Taylor K., Harris D.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
EMBL: U00001.
DR Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=1161;
RX MEDLINE=97435544; PubMed=9290243;
RA Tait E., Simon M.C., King S., Brown A.J., Gow N.A.R., Shaw D.J.;
RT "A Candida albicans genome project: cosmid contigs, physical mapping,
and gene isolation.";
RL Fungal Genet. Biol. 21:308-314(1997).

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 31, 2001, 16:30:13 ; Search time 12.84 Seconds
(without alignments)
1998.237 Million cell updates/sec

Title: US-09-250-083A-2

Perfect score: 3942
Sequence: 1 MSFIDPYOHIVEHQYSHKF.....LSNVEARRFENKEFLSKPKA 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3942	100.0	749	PA2Y_HUMAN	P47712 homo sapien
2	3793	96.2	749	PA2Y_HORSE	O77793 equus caball
3	3752	95.2	752	PA2Y_RAT	P50393 rattus norv
4	3746.5	95.0	748	PA2Y_MOUSE	P47713 mus musculu
5	3391	86.0	748	PA2Y_CHICK	P49147 gallus gall
6	2791	70.8	741	PA2Y_BRARE	P50392 brachydanio
7	232.5	5.9	649	PLB1_NORDE	O11121 torulaspora
8	221.5	5.6	612	PLB1_PENCH	P39457 penicillium
9	219.5	5.6	664	PLB1_YEAST	P39105 saccharomyc
10	207.5	5.3	706	PLB2_YEAST	O03674 saccharomyc
11	205.5	5.2	686	PLB3_YEAST	O08108 saccharomyc
12	148.5	3.8	536	SPO1_YEAST	P53541 saccharomyc
13	134	3.4	658	KPC1_LYPTI	O25378 lytechinus
14	128	3.2	684	RP3A_RAT	P47709 rattus norv
15	125	3.2	704	RP3A_BOVIN	O06846 bos taurus
16	122.5	3.1	854	VG12_BPH2	P20345 bacterioph
17	122	3.1	3829	SACS_HUMAN	O9n214 homo sapien
18	118.5	3.0	664	YFGK_CAEEL	O18696 caenorhabd
19	116.5	3.0	1216	P1B1_RAT	P10687 rattus norv
20	116	2.9	503	CP33_HUMAN	P05184 homo sapien
21	116	2.9	606	RP3A_MOUSE	P47708 mus musculu
22	116	2.9	1234	P1P3_MOUSE	P51432 mus musculu
23	115.5	2.9	1216	P1B1_BOVIN	P10894 bos taurus
24	115	2.9	970	T3RE_BPP1	O9n666 bacterioph
25	113.5	2.9	1216	P1B1_HUMAN	O9n666 homo sapien
26	113.5	2.9	3830	SACS_MOUSE	O9j168 mus musculu
27	112	2.8	2464	MAPR_MOUSE	P14873 mus musculu
28	111.5	2.8	697	KPCG_HUMAN	P05129 homo sapien
29	111.5	2.8	697	KPCG_RABIT	P10829 oryctolopha
30	111.5	2.8	854	VG12_BPP2A	P07537 bacterioph
31	111	2.8	1815	UN13_CAEEL	P27715 caenorhabd
32	110.5	2.8	502	CP34_HUMAN	P08664 homo sapien
33	110.5	2.8	639	KPC1_DROME	P05130 drosophila

34	110.5	2.8	682	1	KPCG_BOVIN	P05128 bos taurus
35	108.5	2.8	422	1	SYT2_MOUSE	P46097 mus musculu
36	108.5	2.8	697	1	KPCG_MOUSE	P05697 mus musculu
37	108.5	2.8	1071	1	TRI_THEAC	P96086 thermoplasm
38	108	2.7	897	1	EP15_MOUSE	P42567 mus musculu
39	107.5	2.7	590	1	ASNS_ORYSA	O43011 oryza sativ
40	107	2.7	644	1	ARNT_DROME	O15945 drosophila
41	107	2.7	688	1	ARNT_RAT	P26819 rattus norv
42	107	2.7	1039	1	YLK6_CAEEL	P41954 caenorhabd
43	106.5	2.7	543	1	APPA_BACSU	P42061 bacillus su
44	106	2.7	672	1	KPCG_HUMAN	P17252 homo sapien
45	106	2.7	1676	1	COS_HUMAN	P01031 homo sapien

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	749 AA.
PA2Y_HUMAN				
ID	P47712;			
AC	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE); LYSOPHOSPHOLIPASE (EC 3.1.1.5)].			
DE	PLA2G4 OR CPLA2.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=91256305; PubMed=1904318; Ramsha C.S., Sultzman L.A., Clark J.D., Lin L.-L., Kriz R.W.,			
RA	Lin A.Y., Milona N., Knopf J.L.;			
RT	"A novel arachidonic acid-selective cytosolic PLA2 contains a Ca(2+)-dependent translocation domain with homology to PKC and GAP.";			
RL	Cell 65:1043-1051(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91331987; PubMed=1869522;			
RA	Sharp J., White D., Chlou G., Goodson T., Gamboa G., McClure D., Burgess E., Hoskins J., Skatrud P., Sportsman J., Becker G., Kang L., Roberts E., Kramer R.;			
RT	"Molecular cloning and expression of human Ca(2+)-sensitive cytosolic phospholipase A2.";			
RL	J. Biol. Chem. 266:14850-14853(1991).			
RN	[3]			
RP	MUTAGENESIS OF SER-505, AND PHOSPHORYLATION BY MAP KINASE.			
RX	MEDLINE=93145328; PubMed=8381049;			
RA	Lin L.-L., Wartmann M., Lin A.Y., Knopf J.L., Seh A., Davis R.J.;			
RT	"CPLA2 is phosphorylated and activated by MAP kinase.";			
RL	Cell 72:269-278(1993).			
RN	[4]			
RP	MUTAGENESIS OF SER-228.			
RX	MEDLINE=9429545; PubMed=8027085;			
RA	Sharp J.D.,			
RT	Unpublished results, cited by:			
RL	Nalefski E.A., Sultzman L.A., Martin D.M., Kriz R.W., Towler P.S., Knopf J.L., Clark J.D.;			
RL	J. Biol. Chem. 269:18239-18249(1994).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 16-141.			
RX	MEDLINE=98104145; PubMed=9430701;			
RA	Perisic O., Fong S., Lynch D.E., Bycroft M., Williams R.L.;			
RT	"Crystal structure of a calcium-phospholipid binding domain from cytosolic phospholipase A2.";			
RL	J. Biol. Chem. 273:1596-1604(1998).			
RN	[6]			
RP	STRUCTURE BY NMR OF 1-138.			
RX	MEDLINE=98332749; PubMed=9665851;			

RA	Xu G.-Y., McConagh T., Yu H.-A., Nalefski E.A., Clark J.D.,
Rt	Cunning D.A.:
Rt	*Solution structure and membrane interactions of the C2 domain of
Rt	cytosolic phospholipase A2.*
RL	J. Mol. Biol. 280:485-500(1998).
CC	-1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE
CC	SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
CC	LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
CC	THE INFLAMMATORY RESPONSE.
CC	-1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGlyceryl-
CC	phosphocholine + A FATTY ACID ANION.
CC	-1- CATALYTIC ACTIVITY: 2-Lysophosphatidylcholine + H(2)O = GLYCERO-
CC	phosphocholine + A FATTY ACID ANION.
CC	-1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ADP, EGF,
CC	THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE
CC	VESSICLES IN A CALCIUM-DEPENDENT FASHION.
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES SUCH AS
CC	MACROPHAGES, PLATELETS, NEUTROPHILS, FIBROBLASTS AND LUNG
CC	ENDOTHELIUM.
CC	-1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
CC	MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
CC	ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
CC	CYTOSOLIC CA2+.
CC	-1- PM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE.
CC	-1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC	-----
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CC	or send an email to license@isb-sib.ch)
CC	-----
DR	EMBL; M72393; AAB00789.1; .;
DR	EMBL; M68874; AAA60105.1; .;
DR	PIR; A39329; A39329.
DR	PDB; IRMW: 25-FEB-98.
DR	PDB; IBCI: 13-JAN-99.
DR	MIM; 600522; .;
DR	InterPro; IPR000008; .;
DR	InterPro; IPR002642; .;
DR	pfam; PF00168; C2; 1.
DR	pfam; PF01735; PLA2_B; 1.
DR	PROSITE; PS50004; C2_DOMAIN_2; 1.
KW	Hydrolase; Lipid degradation; Calcium; Phosphorylation; 3D-structure.
FT	DOMAIN 1 178
FT	DOMAIN 5 106
FT	MOD_RES 505 505
FT	MUTAGEN 228 228
FT	MUTAGEN 505 505
FT	MUTAGEN 505 505
SO	SEQUENCE 749 AA; 85210 MW; 3F9CDD5A98231C70 CNC64; RELEASE OF ARACHIDONIC ACID.

Query Match	100.0%	Score 39423	DB 1	Length 749
Best Local Similarity	100.0%	Pred. No. 3,1e-276		
Matches 749	Conservative	0	Mismatches 0	Indels 0
				Gaps 0
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Db	1	MSFIDPQHIILYEHQYSHKFTVVLVRATVVTGAGCDMLDPDPYVELEISTTPDSRKT	60	
QY	61	RHFNDINPVNNEFEFILLDPQENVLEITLMDANYVMDLTGATFTVSSMKVGEKEY	120	
Db	61	RHFNDINPVNNEFEFILLDPQENVLEITLMDANYVMDLTGATFTVSSMKVGEKEY	120	
QY	121	PIFIHQVEMVLEMSLEVCSPDLRFSMALCQOERTFRQQRKEHIRESKKLLGPRNSG	180	
Db	121	PIFIHQVEMVLEMSLEVCSPDLRFSMALCQOERTFRQQRKEHIRESKKLLGPRNSG	180	

Qy	181	LHSADYVVAIIILSGGGEFRAMVGEQVMKALYESGILDCATYAGISGSTMWSTLYSH	240
Db	181	LHSADYVVAIIILSGGGEFRAMVGEQVMKALYESGILDCATYAGISGSTMWSTLYSH	240
Qy	241	PDFPEKGPEELINEELMKVSNPLLLLTPOKVRKYVESLWKKKSSGQPVFTDIFGMLIG	3000
Db	241	PDFPEKGPEELINEELMKVSNPLLLLTPOKVRKYVESLWKKKSSGQPVFTDIFGMLIG	3000
Qy	301	ETLIHNRNNTLLSLKEKVNTAQCPDLPFTCLHVKPDVSELMFADWVESPYEIGMAKYG	360
Db	301	ETLIHNRNNTLLSLKEKVNTAQCPDLPFTCLHVKPDVSELMFADWVESPYEIGMAKYG	360
Qy	361	TEMAPDLGSKFEMFGTYKKRKEENPLHFMGMWSAPESILFNRLVAGSSGOSRSTHEE	420
Db	361	TEMAPDLGSKFEMFGTYKKRKEENPLHFMGMWSAPESILFNRLVAGSSGOSRSTHEE	420
Qy	421	LENTTKHIVNSDSDSDDESHPEKGTENEDAGSDYSDQNASVHIMIMALVSDSALFN	480
Db	421	LENTTKHIVNSDSDSDDESHPEKGTENEDAGSDYSDQNASVHIMIMALVSDSALFN	480
Qy	481	TREGRAGVHNHFMGLNINTSYPLSPUSDATODSEFDDEIDAADVPDEFERIYEPIDV	540
Db	481	TREGRAGVHNHFMGLNINTSYPLSPUSDATODSEFDDEIDAADVPDEFERIYEPIDV	540
Qy	541	KSKKHHVDSGLTFENLPPLRLRQRGVDLISDFSARSDSSPPKELLLEKMAKMN	600
Db	541	KSKKHHVDSGLTFENLPPLRLRQRGVDLISDFSARSDSSPPKELLLEKMAKMN	600
Qy	601	KLPEFKIDPYVFDREGLKECVYFKPKNPDMEDCPTIIHFLVLANINFRKAKAGVPRETE	660
Db	601	KLPEFKIDPYVFDREGLKECVYFKPKNPDMEDCPTIIHFLVLANINFRKAKAGVPRETE	660
Qy	661	EKEKEIADFDIDDESPSTFENFOYPMQAEKRLHDLMHFNTLNNIDVIKEMAVESIEYRR	720
Db	661	EKEKEIADFDIDDESPSTFENFOYPMQAEKRLHDLMHFNTLNNIDVIKEMAVESIEYRR	720
Qy	721	QNPSCRVSJLSNVARFRFNKEFLSKRPA 749	
Db	721	QNPSCRVSJLSNVARFRFNKEFLSKRPA 749	

RESULT	2
PAZY_HORSE	
ID	PAZY_HORSE
STANDARD;	PRT; 749 AA.
AC	077993.
DT	15-JUL-1999 (Rel. 38, Created)
DT	15-JUL-1999 (Rel. 38, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	CYCLOSLIC PHOSPHOLIPASE A2 (CP1A2) [INCLUDES: PHOSPHOLIPASE A2
DE	(EC 3.1.1.4) (CP1A2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE);
DE	LYSOPHOSPHOLIPASE (EC 3.1.1.5)].
GN	PLA2G4 OR CPLA2.
OS	Equus caballus (Horse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX	NCBI_TaxID=9796;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Neutrophils.
RA	Larsson Persell P.K.A., Lindberg A., Karlsson S., Lindgren J.A.,
RA	Claesson H.E.;
RT	"Purification, characterization and cDNA sequencing of calcium-
RT	dependent cycloslolic phospholipase A2 from equine neutrophils.";
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBD databases.
CC	-1 FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE
CC	SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
CC	LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
CC	THE INFLAMMATORY RESPONSE.
CC	-1 CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1-ACYLGLYCERYL-
CC	PHOSPHOCHOLINE + A FATTY ACID ANION.
CC	-1 CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O -> GLYCERO-
CC	PHOSPHOCHOLINE + A FATTY ACID ANION.
CC	-1 ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,

```

CC THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+ (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE
CC VESICLES IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).
CC -1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
CC MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
CC ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
CC CYTOSOLIC CA2+ (BY SIMILARITY).
CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY
CC SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -----
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CC -----
CC DR EMBL: AF092539; AAC61774.1; -.
CC DR InterPro: IPR000008; -.
CC DR InterPro: IPR002642; -.
CC DR Pfam: PF00168; C2_1;
CC DR Pfam: PF01735; PLA2_B_1.
CC DR PROSITE: PS50004; C2_DOMAIN_2; 1.
CC KM Hydrolyase; lipid degradation; calcium; phosphorylation.
CC FT DOMAIN 1 178 PHOSPHOLIPID BINDING (PROBABLE).
CC FT MOD_RES 5 106 C2 DOMAIN.
CC FT MOD_RES 505 505 PHOSPHORYLATION (BY MADK) (BY
CC SIMILARITY).
CC SQ SEQUENCE 749 AA; 85454 MW; 493a67DF28D50FE0 CRC64;

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Query Match 96.2%; Score 3793; DB 1; Length 749;
 Best Local Similarity 95.38; Pred. No. 1.7e-265;
 Matches 744; Conservative 24; Mismatches 11; Indels 0; Gaps 0;

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QY 1 MSFIDPQHIIVEHOXSHKFTVVVLRATKYKAGFGMDLTPPYVELFISTPPDSKRT 60
DB 1 MSFIDPQHIIVEHOXSHKFTVVVLRATKYKAGFGMDLTPPYVELFISTPPDSKRT 60
QY 61 RHNNDINPVWNETFEFLDPNOENVLEITLMDANYMDETLGTATVSSMKVGEKREY 120
DB 61 RHNNDINPVWNETFEFLDPNOENVLEITLMDANYMDETLGTATVSSMKVGEKREY 120
QY 121 PFTFNQVTEVLMSELEVCSPDLRFSMALCDEKTPROQRKEHRRSMKKLLGPKRSEG 180
DB 121 PFTFNQVTEVLMSELEVCSPDLRFSMALCDEKTPROQRKEHRRSMKKLLGPKRSEG 180
QY 181 LHSARDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCATVYAGLSGTSWYSTLYSH 240
DB 181 LYSTRDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCATVYAGLSGTSWYSTLYSH 240
QY 241 PDPEKGPPEINEELMKNSVHNPILLITPQVKRYVESLMKKKSGQVPTFDIFGMLIG 300
DB 241 PDPEKGPPEINEELMKNSVHNPILLITPQVKRYVESLMKKKSGQVPTFDIFGMLIG 300
QY 301 ETIHNHNMNTLSLKKKVTACQPLPLFTCLHKKPVSELMFADWVEFSPEYEGMAKYG 360
DB 301 ETIHNHNMNTLSLKKKVTACQPLPLFTCLHKKPVSELMFADWVEFSPEYEGMAKYG 360
QY 361 TFMAPDLFGSKFPMGTGVVKKYEENPLHFLMGVGSASFILFNRYLGVSGSQSRGSTMEEE 420
DB 361 TFMAPDLFGSKFPMGTGVVKKYEENPLHFLMGVGSASFILFNRYLGVSGSQSRGSTMEEE 420
QY 421 LEMITTKHIVSNDSDSDSHPEKGTENDAGSDIOSDNQASHIRMAIVLSDSALFN 480
DB 421 LEMITTKHIVSNDSDSDSHPEKGTENDAGSDIOSDNQASHIRMAIVLSDSALFN 480
QY 481 TRGGRAGKYNFMGLNLNMFPLSDFAQDSFDDDELDAVAVNDPDEFERYEPLDY 540
DB 481 TRGGRAGKYNFMGLNLNMFPLSDFAQDSFDDDELDAVAVNDPDEFERYEPLDY 540

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QY 541 KSKKIHVDSGLTFENLPYLILRPORCVDLISFDSARPSSDPPKELLAEKNAKM 600
DB 541 KSKKIHVDSGLTFENLPYLILRPORCVDLISFDSARPSSDPPKELLAEKNAKM 600
QY 601 KLPEPKIDPVYDFREGIEKCYVERKPNKDMEKDCPTIIHFVLNINFRKYKAGVPRETE 660
DB 601 KLPEPKIDPVYDFREGIEKCYVERKPNKDMEKDCPTIIHFVLNINFRKYKAGVPRETE 660
QY 661 EKEEIAFDIFDDPESFSTFNQYPMQAKRLDLMHFNTLNNIDVYKAMVESIEYR 720
DB 661 EKEEIAFDIFDDPESFSTFNQYPMQAKRLDLMHFNTLNNIDVYKAMVESIEYR 720
QY 721 QNPSRCSVLSNVEARFPFKNEFLSKPKA 749
DB 721 QNPSRCSVLSNVEARFPFKNEFLSKPKA 749

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RESULT 3
 PAZY_RAT
 ID PAZY_RAT STANDARD; PRT; 752 AA.
 AC P50393;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2
 DE (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE);
 GN PLA2G4 OR CPLA2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Owada Y., Tomioka T., Yoshimoto T., Kondo H.;
 RT "Molecular cloning of rat cDNA for cytosolic phospholipase A2 and the
 RT increased gene expression in the dentate gyrus following transient
 RT forebrain ischemia.";
 RL Brain Res. Mol. Brain Res. 25:364-368(1994).
 RN [2]
 RP ERRATUM.
 RC MEDLINE=95206125; PubMed=7898324;
 RA Owada Y., Tomioka T., Yoshimoto T., Kondo H.;
 RL Brain Res. Mol. Brain Res. 27:355-355(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Pancreatic Islets;
 RA MEDLINE=98223459; PubMed=9555100;
 RA Ma Z., Ramanadham S., Hu Z., Turk J.;
 RT "Cloning and expression of a group IV cytosolic Ca2+-dependent
 RT phospholipase A2 from rat pancreatic islets. Comparison of the
 RT expressed activity with that of an islet group VI cytosolic Ca2+-
 RT independent phospholipase A2.";
 RL Biochim. Biophys. Acta 1391:384-400(1998).
 CC -1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE
 CC SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
 CC LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
 CC THE INFLAMMATORY RESPONSE.
 CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O - 1-ACYLGLYCERYL-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O = GLYCERO-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,
 CC THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE
 CC VESICLES IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: IN BRAIN TISSUE, EXPRESSED IN LOW LEVELS IN
 CC OLFACTORY MITRAL AND GRANULE CELLS, IN HIPPOCAMPAL PYRAMIDAL
 CC CELLS AND IN DENTATE AND CEREBELLAR GRANULE CELLS.
 CC -1- INDUCTION: LEVELS OF RAT CPLA2 ARE INCREASED IN DENTATE GRANULE
 CC CELLS DURING ISCHEMIA.

CC	-1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF CYTOSOLIC CA2+ (BY SIMILARITY).
CC	-1- PPM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY SIMILARITY).
CC	-1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC	-----
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CC	or send an email to license@isb-sib.ch .
CC	-----
DR	EMBL; S77829; AAB33847.1; -.
DR	EMBL; U38376; AAC21591.1; -.
DR	HSSP; P47712; IBCI.
DR	InterPro; IPRO00008; -.
DR	InterPro; IPRO02642; -.
DR	Pfam; PF00168; C2; 1.
DR	Pfam; PF01735; PLA2_B; 1.
DR	PROSITE; PS50004; C2_DOMAIN_2; 1.
KW	Hydrolase; Lipid degradation; Calcium; Phosphorylation.
RN	DOMAIN 1 178
FT	DOMAIN 5 106
FT	MOD_RES 505 505
FT	-----
FT	SIMILARITY:
FT	C -> S (IN REF. 3).
FT	R -> Q (IN REF. 3).
FT	Q -> L (IN REF. 3).
FT	MST -> IVP (IN REF. 3).
FT	S -> L (IN REF. 3).
FT	E -> V (IN REF. 3).
FT	P -> T (IN REF. 3).
FT	SEQUENCE 752 AA; 85706 MW; CB8F71B05FBF732 CRC64;

[illegible]

Db	421	LENTAKHIVSDSDDEAQQGPKGTENEDAREYQNDQNASVWHRLMALVPSALFN	480
Qy	481	TREGAGAVHNFMGLNNTSYPLSPLEDFATQDSFDDDELDAAVADDEPRITPELDV	540
Db	481	TREGAGKEHNFMGLNNTSYPLSPLEDFSPQDSFDDDELDAAVADDEPRITPELDV	540
Qy	541	KSKRHHVDSGTFNLPPLILRPGVDLIISPFESARPSDSSPPFKELLAEKMAKN	600
Db	541	KSKRHHVDSGTFNLPPLILRPGVDLIISPFESARPSDSSPPFKELLAEKMAKN	600
Qy	601	KLPEFKIDPYFDRGLCECYVFKRNKNDMEKDCPTIIHFVLNINFRKYAPGVRETE	660
Db	601	KLPEFKIDPYFDRGLCECYVFKRNKNDMEKDCPTIIHFVLNINFRKYAPGVRETE	660
Qy	661	EKEETADFDIDDEPSPSTFNFOYPNQAFKRLDLMHFNLTNLNIDVTEKAVESIEYR	720
Db	661	EKEETADFDIDDEPSPSTFNFOYPNQAFKRLDLMHFNLTNLNIDVTEKAVESIEYR	720
Qy	721	QNPSCSVSLSNVEARFRFNKEFLSKPRA	749
Db	721	QNPSCSVSLSNVEARFRFNKEFLSKPRA	749
RESULT 4			
PA2Y-MOUSE	PA2Y-MOUSE	STANDARD:	PRT: 748 AA.
AC	PA47713;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	15-JUN-1999 (Rel. 38, Last annotation update)		
DE	CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2		
DE	(EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACETYLHOLASE);		
DE	LYSOPHOSPHOLIPASE (EC 3.1.1.5)].		
GN	PLA2G4 OR CPLA2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
ON	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91256305; PubMed=1904318;		
RA	Clark J.D., Lin L.-L., Kriz R.W., Ramesha C.S., Soltzman L.A.,		
RA	Lin A.Y., Milona N., Knopf J.L.;		
RT	A novel arachidonic acid-selective cytosolic PLA2 contains a Ca(2+)-		
RT	dependent translocation domain with homology to PKC and GAP.";		
RL	Cell 65:1043-1051(1991).		
CC	-1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE		
CC	SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS		
CC	LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF		
CC	THE INFLAMMATORY RESPONSE.		
CC	-1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-		
CC	PHOSPHOCHOLINE + A FATTY ACID ANION.		
CC	-1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O = GLYCERO-		
CC	PHOSPHOCHOLINE + A FATTY ACID ANION.		
CC	-1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,		
CC	THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.		
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC. TRANSLOCATES TO MEMBRANE		
CC	VESICLES IN A CALCIUM-DEPENDENT FASHION.		
CC	-1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID		
CC	MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE		
CC	ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF		
CC	CYTOSOLIC CA2+ (BY SIMILARITY).		
CC	-1- PPM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY		
CC	SIMILARITY).		
CC	-1- SIMILARITY: CONTAINS 1 C2 DOMAIN.		
CC	-----		
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CC	entities requires a license agreement. (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		

CC EMBL: M72394; AAB00796.1; -.
 DR HSSP; P47712; IBCI.
 DR MGD; MGI:1195256; Pla2g4.
 DR InterPro: IPR000008; -.
 DR InterPro: IPR002642; -.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF01735; PLA2_B; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR HydroLase: Lipid degradation; Calcium; Phosphorylation.
 FT DOMAIN 1 178 PHOSPHOLIPID BINDING (PROBABLE).
 FT MOD_RES 5 106 C2 DOMAIN.
 FT MOD_RES 505 305 PHOSPHORYLATION (BY MAPK) (BY
 SIMILARITY).
 SQ SEQUENCE 748 AA; 85222 MW; 49D12BB2911492A CRC64;

Query Match 95.0%; Score 3746.5; DB 1; Length 748;
 Best Local Similarity 94.8%; Pred. No. 3.8e-262;
 Matches 708; Conservative 24; Mismatches 14; Indels 1; Gaps 1;

QY 1 MSFIDPQHIIIVEHQYSHKFTVYVLRATKYTGAFGMDLPDPYVELEISTPDSRRRT 60
 |||||||
 DB 1 MSFIDPQHIIIVEHQYSHKFTVYVLRATKYTGAFGMDLPDPYVELEISTPDSRRRT 60
 QY 61 RHFNNDINPVWNETFEELDPNENVEITLMDANYVDETLGATFTVSMKVGKKEV 120
 |||||||
 DB 61 RHFNNDINPVWNETFEELDPNENVEITLMDANYVDETLGATFTVSMKVGKKEV 120
 QY 121 PFITNOTENVLEMSLVSCPDRLRFSMALCDOKETROQKEIRRESMKLLQPKKSEG 180
 |||||||
 DB 121 PFITNOTENVLEMSLVSCPDRLRFSMALCDOKETROQKEIRRESMKLLQPKKSEG 180
 QY 121 PFITNOTENVLEMSLVSCPDRLRFSMALCDOKETROQKEIRRESMKLLQPKKSEG 180
 |||||||
 DB 121 PFITNOTENVLEMSLVSCPDRLRFSMALCDOKETROQKEIRRESMKLLQPKKSEG 180
 QY 181 LHSARDPVVAIIIGSGGFRAMVFGSCVMKALYESGILDCATYAGLSGTSWYSTLYSH 240
 |||||||
 DB 181 LYSRDVPAVAIIIGSGGFRAMVFGSCVMKALYESGILDCATYAGLSGTSWYSTLYSH 240
 QY 241 PDPEKPEEINELMKNVSHNPLLLLPQKRYVESLWKKKSGQPVTFDIFGMLIG 300
 |||||||
 DB 241 PDPEKPEEINELMKNVSHNPLLLLPQKRYVESLWKKKSGQPVTFDIFGMLIG 300
 QY 301 ETLIHNMNTLSLKKKVTVAOCPLPLFTCLHYKPDVSELMFADWVEFSYEIGMAKYG 360
 |||||||
 DB 301 ETLIHNMNTLSLKKKVTVAOCPLPLFTCLHYKPDVSELMFADWVEFSYEIGMAKYG 360
 QY 361 TFMAPDLFGSKFEMGYVKKYEENPLHFLMGVGSASFILFNRYLGVSGSGSSTMEEE 420
 |||||||
 DB 361 TFMAPDLFGSKFEMGYVKKYEENPLHFLMGVGSASFILFNRYLGVSGSGSSTMEEE 420
 QY 421 LENTTTHIVSNDSDSDSHKPGTENEDAGSDYQSDNOASWIHMALVSDSALFN 480
 |||||||
 DB 421 LENTTTHIVSNDSDSDSHKPGTENEDAGSDYQSDNOASWIHMALVSDSALFN 480
 QY 481 TREBRACKVNHFMGLNLSYPLSLSDPATQSDPDDDELDAAVADPEERIEPELDV 540
 |||||||
 DB 481 TREBRACKVNHFMGLNLSYPLSLSDPATQSDPDDDELDAAVADPEERIEPELDV 540
 QY 541 KSKRIHYVDSGLFENLPYPLILRPGRGVDLISDFGARSPPSPPEKELLAKMKMN 600
 |||||||
 DB 541 KSKRIHYVDSGLFENLPYPLILRPGRGVDLISDFGARSPPSPPEKELLAKMKMN 600
 QY 540 KSKRIHYVDSGLFENLPYPLILRPGRGVDLISDFGARSPPSPPEKELLAKMKMN 599
 |||||||
 DB 540 KSKRIHYVDSGLFENLPYPLILRPGRGVDLISDFGARSPPSPPEKELLAKMKMN 599
 QY 601 KLPPKIDPVYFDEGLKECVFKPKNPDMKDCPTIIHFVLANINFRKYKAPCVPRETE 660
 |||||||
 DB 601 KLPPKIDPVYFDEGLKECVFKPKNPDMKDCPTIIHFVLANINFRKYKAPCVPRETE 660
 QY 661 EEKRIAPDIFDDPSPSPFNPNQAKRLDLMLHFNLANIDVYKEMVSIETERR 720
 |||||||
 DB 661 EEKRIAPDIFDDPSPSPFNPNQAKRLDLMLHFNLANIDVYKEMVSIETERR 720
 QY 721 QNPSRCSVLSNVEARFPNKEFLSKP 747
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 DB 721 QNPSRCSVLSNVEARFPNKEFLSKP 746
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RESULT 5
 PAZY CHICK STANDARD; PRT; 748 AA.
 ID PAZY CHICK
 AC PA9147;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CYTOSOLIC PHOSPHOLIPASE A2 (CPLA2) [INCLUDES: PHOSPHOLIPASE A2
 DE (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE);
 DE LYSOPHOSPHOLIPASE (EC 3.1.1.5)].
 GN PLA2G4 OR CPLA2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=94299545; PubMed=8027085;
 RA Nalefski E.A., Sultzman L.A., Martin D.M., Kriz R.W., Towler P.S.,
 RA Knopf J.L., Clark J.D.;
 RT "elination of two functionally distinct domains of cytosolic
 RT phospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain
 RT and a Ca(2+)-independent catalytic domain.";
 RL J. Biol. Chem. 269:18239-18249(1994).
 CC -1- FUNCTION: SELECTIVELY HYDROLYZES ARACHIDONYL PHOSPHOLIPIDS IN THE
 CC SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
 CC LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
 CC THE INFLAMMATORY RESPONSE.
 CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O - 1-ACYLGLYCERYL-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O - GLYCERO-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,
 CC THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.
 CC -1- SUBCELLULAR LOCATION: CYTOSOL/MIC. TRANSDUCES TO MEMBRANE
 CC VESICLES IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).
 CC -1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
 CC MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
 CC ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
 CC CYTOSOLIC CA2+ (BY SIMILARITY).
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.

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DR EMBL: U10329; AAA53228.1; -.
 DR HSSP; P47712; IBCI.
 DR InterPro: IPR000008; -.
 DR InterPro: IPR002642; -.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF01735; PLA2_B; 1.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR HydroLase: Lipid degradation; Calcium; Phosphorylation.
 FT DOMAIN 1 178 PHOSPHOLIPID BINDING.
 FT MOD_RES 5 106 C2 DOMAIN.
 FT MOD_RES 505 305 PHOSPHORYLATION (BY MAPK) (BY
 SIMILARITY).
 SQ SEQUENCE 748 AA; 84978 MW; 996A5256CA032F75 CRC64;

Query Match 86.0%; Score 3391; DB 1; Length 748;
 Best Local Similarity 83.9%; Pred. No. 1.5e-236;
 Matches 625; Conservative 64; Mismatches 56; Indels 0; Gaps 0;

```

RA Malfak E.A., Sulteman L.A., Martin D.M., Kitz R.W., Towler P.S.,
RT Knopf J.L., Clark J.D.;
RT "Delineation of two functionally distinct domains of cytosolic
RT phospholipase A2, a regulatory Ca(2+)-dependent lipid-binding domain
RT and a Ca(2+)-independent catalytic domain.";
RL J. Biol. Chem. 269:18239-18249(1994).
CC -1- FUNCTION: SELECTIVELY HYDROLYSES ARACHIDONYL PHOSPHOLIPIDS IN THE
CC SN-2 POSITION RELEASING ARACHIDONIC ACID. TOGETHER WITH ITS
CC LYSOPHOSPHOLIPID ACTIVITY, IT IS IMPLICATED IN THE INITIATION OF
CC THE INFLAMMATORY RESPONSE.
CC -1- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O = 1-ACYLGLYCERYL-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)O = GLYCERO-
CC PHOSPHOCHOLINE + A FATTY ACID ANION.
CC -1- ENZYME REGULATION: STIMULATED BY AGONISTS SUCH AS ATP, EGF,
CC THROMBIN AND BRADYKININ AS WELL AS BY CYTOSOLIC CA2+.
CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC. TRANSLOCATES TO MEMBRANE
CC VESICLES IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).
CC -1- DOMAIN: THE N-TERMINAL C2 DOMAIN, BY ITS ASSOCIATION WITH LIPID
CC MEMBRANES, MEDIATES THE REGULATION OF CPLA2 BY PRESENTING THE
CC ACTIVE SITE TO ITS SUBSTRATE IN RESPONSE TO ELEVATIONS OF
CC CYTOSOLIC CA2+ (BY SIMILARITY).
CC -1- PMM: ACTIVATED BY PHOSPHORYLATION ON A SERINE RESIDUE (BY
CC SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U10330; AAA53229.1; -.
DR HSSP; P47712; IBC1.
DR ZFIN; ZDB-GENE-990415-45; cpla2.
DR InterPro; IPR000008; -.
DR InterPro; IPR002642; -.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF01735; PLA2_B; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
KW Hydrolase; Lipid degradation; Calcium; Phosphorylation.
FT DOMAIN 1 172 PHOSPHOLIPID BINDING (PROBABLE).
FT 1 100 C2 DOMAIN
FT MOD_RES 498 498 PHOSPHORYLATION (BY MAPK) (BY
FT SIMILARITY).
FT FT FT
SQ SEQUENCE 741 AA; 83809 MM; 34896B1A8364A9D4 CRC64;

Query Match 70.8%; Score 2791; DB 1; Length 741;
Best Local Similarity 72.7%; Pred. No.2.5e-193;
Matches 537; Conservative 81; Mismatches 111; Indels 10; Gaps
7;

9 HIIYHQYSHFETVVVLTATKVTGCAFGDMDLTPDYVELFISTPDSKRTAHNNDIN 68
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3 NIIYHQYSHRLKTLVVAENVTGCAFGDLDTPDYVELSVPTPESKRRTAHNNDIN 62

69 PYWNTFEFILLDPNOENVLETTIMDANYVMDLTGTAFTVSSMAVGEKKVPEFFNOYT 128
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
63 PKWNTFEFILLDPNOSNVLEVTIMDANYVMDLTGTAFTVSSKTLVVAOMENHTLSIGTFT 122

129 EYVLEMSLEVSCPLRFSMALCDEKEFPQORKEHIRESMKLLGPKNSEGLISA-RDV 187
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
123 KYFDLILLEVCASTDLRKFSMTLCDEKLFMQRTRRNVMLSTIKLLKMENPRLPSPPREV 182

188 PYVALIGSGGGERANVGFSGVNAKALYESGILDCAITYVAGLSGSITWYMSLTLYSHDPPEKG 247
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
183 PLTALIGSGGGERANVGFSGVNAKALYESGVECDATYVAGLSGSITWYMSLTLYSHDPPEKAG 242

248 PBEINBELMKVSNHPDLLLPQAKRKYVESIMKKKSSGQPYTFDIDGMLIGETLLINR 307
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
243 PGDIIKELMKNRNSNPDLTLPLPQINNRVKAIMKKKSGQPYTFDIDGMLIGETLLIGR 302

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Db 255 -----FFVF-----ONAKMP-----PIYADGRYP-----GTRKVINLNAV- 286
 QY 380 KYEENPLHFLMGWGSASFSLFN-RVLGVSGSGSGSTMEELENTTKHIVNSDSSD 438
 Db 287 -FEENP--FEKGSMDPSLNSFANKYIGT--NNSNGVPLE----- 321
 QY 439 DESHEPKGTENEDAGSDYQSDNQASWIRHIMALVSDALFNTREGRAKHNFMGLNL 498
 Db 322 -----RGKCT-----AGFD-----NAGFI-----MGTSSTLFN-----QLLRIN- 351
 QY 499 NTSP--LSPLSDPAFQDSFDDDELDAVADPDEF-----ERYEPLDKSKKIHVVS 550
 Db 352 STLHPSPFTFLARHFLKD-LSODFNDAVYSPNPKDKTKELSDYTSIVSDSLFLVDG 410
 QY 551 GL--TFNLPYPLILRPGRGVLLISFDSARPSSPPFKELL--LAEKMAKMK-LPFPK 606
 Db 411 GEDDENPVLPLQKEKDVDITFAVNSADMRLKMPDGSLSVHTYERQFQOGMSFPY 470
 QY 607 I-DEYVEDREGLEKCYFKP-----KNPDMKDCPTIHFVLANINFRKYPAGVPR 657
 Db 471 VPDNTFVNMLGNK-----KTFEGCDANNLTDQYIPPLVYLPMAYSPFNSNGAFKLS 526
 QY 658 ETEEEK-----ELDPDIF-DDPE 675
 Db 527 YSEQRSMIONGFEIATRNFTDDE 553

RESULT 12
 ID SP01_YEAST STANDARD; PRT; 536 AA.
 AC P53541;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SPOILATION PROTEIN SP01.
 GN SP01 OR YNL012W OR N2858.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97080530; PubMed=8921875;
 RT Tevazade G.G., Mushagian A.R., Esposito R.E.;
 RT "The SP01 gene product required for meiosis in yeast has a high
 RT similarity to phospholipase B enzymes.";
 RL Gene 177:253-255(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA Andre B., Iraqi Housaini I., Urrestazu L.A., Vissers S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: REQUIRED FOR MEIOSIS.
 CC -!- SIMILARITY: TO FUNGAL LYSOPHOSPHOLIPASES.
 CC -----
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 CC -----
 CC EMBL: L39372; AAB38425.1; -
 DR EMBL: Z71288; CA95872.1; -
 DR SCD: S0004957; SP01.
 DR InterPro: IPR002642; -
 DR Pfam: PFO1735; PLA2_B_1.
 KM Sporulation; Meiosis; lipid degradation; Hydrolase.
 SQ SEQUENCE 536 AA; 61448 MW; 69A03B31189EDDID CRC64;

Query Match 3.8%; Score 148.5; DB 1; Length 536;

Best Local Similarity 19.6%; Pred. No. 0.0036;
 Matches 100; Conservative 63; Mismatches 150; Indels 197; Gaps 19;

QY 202 MWGFGVMAKLYESGILDCAFYVAGLSGMYMSTL----- 237
 Db 2 LVG-TGFIQNDNDGLFEYSDYIAGLSGWIIMDLVYQNEVYKSLQEDMLEDDLLGI 60
 QY 238 ----YSHPDEPEKPEEIN-----EELMKVSH----- 261
 Db 61 PEFDISEELIYNAKKRYNDNDLKKRKQGGSLITSSNPFYEQLEELMNSIEELPEDYMI 120
 QY 262 -----NPLLL-----TPQYKRYVESLW-----KKSSGQPVTTDI 294
 Db 121 TKRNMLNPLARKLIFPNNTFTGTDAKIEFKKVLDFYKSLHKIKRKKEGFOISTDY 180
 QY 295 FGLMIGETL-----IHNRMNTLSLKEKVTATACPLPFLCHLVKPDVSELMFADW 346
 Db 181 WKAIVQRLKKNFDDPNHSFSFKLVNSSKKEKCVPIPIFVANKNGLLSNVIF--- 237
 QY 347 VEEFSPYEIGMAK--YGTFMAPDLGSKRFMGTV---VKYEENPLHFLMGWGSASFILF 401
 Db 238 -EFTPFEGSWENILRLFLVKLPYLGSKIYSGAKKCLNNTD-----LGTITATSSIF 290
 QY 402 NRVLGVSGSGSGSTMEELENTTKHIVNSDSSDSESHPEKGTENEDAGSDYQSDNQ 461
 Db 291 NNVL----- 294
 QY 462 ASWIRHIMALVSDALFNTREGRAKHNFMGLNLTSTYPLSLSDPAFQDSFDDDEL 521
 Db 295 -----IFTMNLASOS-----SRE--AMKALNNVMGI-----FGLEKEIEFISKSDSRLT 338
 QY 522 DAAYADPDEFEERIEPLDVSKKIH--VVDGSLF-FNLPPYLILRPGRGVLLISFPESA 578
 Db 339 DYAVYQGNPFLYLEKXNVNLNKNHLYLVQGGEGENIPLTLVTPREELDIVLVD-SS 397
 QY 579 RPSDSSPPFKELLAEKMAKMKLPPEKID 608
 Db 398 SDIDYENGSKL-----KRIFEKLD 417

RESULT 13
 ID KPC1_LYTP1 STANDARD; PRT; 658 AA.
 AC Q25378;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PROTEIN KINASE C (EC 2.7.1.1-).
 GN PKC1.
 OS Lytechinus pictus (Painted sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinozoa; Euechinozoa; Echinacea; Temnopneurozoa; Tokopneustidae;
 OC Lytechinus.
 OX NCBI_TaxID=7653;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Rakow T.L., Shen S.S.;
 RT "Molecular cloning and characterization of protein kinase C from the
 RT sea urchin Lytechinus pictus.";
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME (BY SIMILARITY).
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.

[illegible]

Search completed: July 31, 2001, 16:33:29
Job time: 196 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 31, 2001, 16:29:13 ; Search time 19.33 Seconds

(without alignments)
2951.616 Million cell updates/sec

Title: US-09-250-083a-2

Sequence: 1 MSFIDPYGHIIIVHQYSHKF.....LSNVEARRRPNKEFLSKPKA 749

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_68:**
2: PIR1:**
3: PIR2:**
4: PIR3:**
5: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3942	100.0	749	1 A39329	phospholipase A2 (
2	3763	95.5	749	1 B39898	cytosolic phosphol
3	3391	86.0	748	1 I50699	phospholipase A2 c
4	2791	70.8	741	2 B54308	cytosolic phosphol
5	494.5	12.5	541	2 T13162	lysophospholipase
6	221.5	5.6	612	2 S29318	lysophospholipase
7	219.5	5.6	664	2 S53037	PLB1 protein - Yea
8	209.5	5.3	754	2 T18238	lysophospholipase
9	207.5	5.3	706	2 S53035	probable lysophosp
10	205.5	5.2	666	2 S66933	hypothetical prote
11	194.5	4.9	623	2 T40991	probable lysophosp
12	192.5	4.9	624	2 T38006	probable lysophosp
13	178.5	4.5	574	2 T51799	GLB1-like protein
14	172.5	4.4	510	2 T50526	CaLB protein - Ara
15	170.5	4.3	613	2 T38007	probable lysophosp
16	169	4.3	644	2 T37800	probable lysophosp
17	163.5	4.1	673	2 T50281	lysophospholipase
18	148.5	3.8	536	2 S62110	anthranilate phosph
19	140.5	3.6	972	2 T47922	alpha-toxin - Clos
20	140.5	3.6	2178	2 S55805	anthranilate phosph
21	138.5	3.5	773	2 T04143	anthranilate phosph
22	135.5	3.4	505	2 T04143	CUB1 protein - tom
23	134.5	3.4	776	2 C96554	unknown protein [i
24	129	3.3	1278	2 A47462	probable DNA-direc
25	128	3.2	681	2 JX0338	rabphilin-3A - mou
26	128	3.2	684	2 T58166	rabphilin-3A - rat
27	128	3.2	1096	1 S62358	inositol 1,4,5-tri
28	126.5	3.2	2104	2 T38774	myosin-3 heavy cha
29	125	3.2	704	2 A48097	rabphilin-3A - bov

30	122.5	3.1	854	1 WMBP22	gene 12 protein -
31	122.5	3.1	1178	2 S54073	probable membrane
32	121.5	3.1	769	2 T49911	anthranilate phosph
33	121	3.1	675	2 T01234	probable anthranil
34	119	3.0	857	2 T04208	probable anthranil
35	119	3.0	2475	2 S35307	polyprotein pp220
36	118.5	3.0	592	2 T50516	Ca2+ dependent 11p
37	118.5	3.0	664	2 T24459	hypothetical prote
38	117.5	3.0	779	2 T01304	hypothetical prote
39	117.5	3.0	1173	2 T51440	alpha-mannosidase-
40	117.5	3.0	1299	2 T24299	hypothetical prote
41	116.5	3.0	1024	2 D81624	exodeoxyribonuclea
42	116.5	3.0	1216	2 A28821	1-phosphatidylinos
43	116.5	3.0	1777	2 T00490	nonstructural prot
44	116	2.9	504	2 A29410	cytochrome P450, g
45	115.5	2.9	1024	2 F86582	exodeoxyribonuclea

ALIGNMENTS

RESULT 1

A39329

C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2000

C:Accession: A39329; A39898; A54198; S68898
R:Sharp, J.D.; White, D.L.; Chou, X.G.; Goodson, T.; Gamboa, G.C.; McClure, D.; Burg

J. Biol. Chem. 266, 14850-14853, 1991
A:Title: Molecular cloning and expression of human Ca(2+)-sensitive cytosolic phospho

A:Reference number: A39329; MUID:91331987
A:Accession: A39329

A:Molecule type: mRNA
A:Residues: 1-749 <SHA>

A:Cross-references: GB:M68874; NID:q190003; PIDN:AAA60105.1; PID:q190004
A:Note: part of this sequence was confirmed by protein sequencing

R:Clark, J.D.; Lin, L.L.; Kriz, R.W.; Ramesha, C.S.; Sultzman, L.A.; Lin, A.Y.; Milon
Cell 65, 1043-1051, 1991

A:Title: A novel arachidonic acid-selective cytosolic PLA-2 contains a Ca(2+)-depende
A:Reference number: A39898; MUID:91256305

A:Accession: A39898
A:Molecule type: mRNA

A:Residues: 1-749 <CLA>
A:Cross-references: GB:M72393; NID:q190006; PIDN:AAB00789.1; PID:q190007

A:Note: part of this sequence was confirmed by protein sequencing
R:Li, B.; Copp, L.; Castelhan, A.L.; Feng, R.; Stahl, M.; Yuan, Z.; Krantz, A.

Biochemistry 33, 8594-8603, 1994
A:Title: Inactivation of a cytosolic phospholipase A-2 by thiol-modifying reagents: c

A:Reference number: A54198; MUID:94304876
A:Accession: A54198

A:Molecule type: protein
A:Residues: 319-338, 'X', 340-345, 'X', 347-358 <LIA>

A:Note: modification of preferred modification site Cys-324 abolished enzymatic activ
R:Gordon, R.D.; Leighton, I.A.; Campbell, D.G.; Cohen, P.; Creaney, A.; Willton, D.C.;

Eur. J. Biochem. 238, 690-697, 1996
A:Title: Cloning and expression of cytosolic phospholipase A(2) (cPLA(2)) and a natur

results in an increase in specific activity.
A:Reference number: S68897; MUID:96300233

A:Accession: S68898
A:Molecule type: protein

A:Residues: 497-507 <GOR>
C:Comment: This cytosolic phospholipase A2 translocates to membrane vesicles in respo

C:Genetics:

A:Gene: GDB:PLA2G4A; PLA2G4
A:Cross-references: GDB:134687; OMIM:600522

A:Map position: 1q25-1q25
C:Superfamily: cytosolic phospholipase A2

C:Keywords: calcium; carboxylic ester hydrolase; cytosol; inflammation; phosphoprotei
F:505/inding site: phosphate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 3942; DB 1; Length 749;
Best Local Similarity 100.0%; Pred. No. 9, 1e-280;

Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSFIDYQHIIVEHOXSHKFTVVVLRATKVTKGAFGMDLTPDPVYELFISTTPDSKRT 60
Db 1 MSFIDYQHIIVEHOXSHKFTVVVLRATKVTKGAFGMDLTPDPVYELFISTTPDSKRT 60
QY 61 RHFNDINPWNTEFEFILDNPQENVEITLMDANYVMDTIGTATFTVSMKVGEKREY 120
Db 61 RHFNDINPWNTEFEFILDNPQENVEITLMDANYVMDTIGTATFTVSMKVGEKREY 120
QY 121 PEFNOVTEVMELEMSCPDLRFSMALCDQEKTFRQKRKEHIRESMKLLGPKNSG 180
Db 121 PEFNOVTEVMELEMSCPDLRFSMALCDQEKTFRQKRKEHIRESMKLLGPKNSG 180
QY 181 LHSARDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCAITYAGLSGTWMTLYSH 240
Db 181 LHSARDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCAITYAGLSGTWMTLYSH 240
QY 241 PDFPEKGPEEINELMKNSHNPDLTLTPQKRYVESLTKKSSGQPVTFDIFGMLIG 300
Db 241 PDFPEKGPEEINELMKNSHNPDLTLTPQKRYVESLTKKSSGQPVTFDIFGMLIG 300
QY 301 ETLIHRMNTTSLSEKVTACPLPLFTCLHVKPDVSELMFADWVEFSPEIGMAKYG 360
Db 301 ETLIHRMNTTSLSEKVTACPLPLFTCLHVKPDVSELMFADWVEFSPEIGMAKYG 360
QY 361 TFMAPDLFGSKFPMGTIVVKKYEENPLHFLMGVGSASFILFNVLGVSQSOSRGSTMEBE 420
Db 361 TFMAPDLFGSKFPMGTIVVKKYEENPLHFLMGVGSASFILFNVLGVSQSOSRGSTMEBE 420
QY 421 LENITTKHIVSNDSSDDESHKPTENEDAGSDYQSDNQASWIRHMTALVSDSALFN 480
Db 421 LENITTKHIVSNDSSDDESHKPTENEDAGSDYQSDNQASWIRHMTALVSDSALFN 480
QY 481 TREGRAGKVNFMGLNLTSTPLSDPATQDSFDDDELDAVAADPDEFERIYEPDLY 540
Db 481 TREGRAGKVNFMGLNLTSTPLSDPATQDSFDDDELDAVAADPDEFERIYEPDLY 540
QY 541 KSKKIHVDSGLTFNLPYLLLRPQGVDLISFDSARPSSDPFKELLAEKAKKN 600
Db 541 KSKKIHVDSGLTFNLPYLLLRPQGVDLISFDSARPSSDPFKELLAEKAKKN 600
QY 601 KLPFPKIDYVDFREGIACGYFVKPNPDMKDCPTIIHFVLANINFRKXKAPGVRETE 660
Db 601 KLPFPKIDYVDFREGIACGYFVKPNPDMKDCPTIIHFVLANINFRKXKAPGVRETE 660
QY 661 EEKEIADFIDDPESPSTFNFQYPNOAFKRLHDLMHFTLNNDIVIKEMVESTIEYR 720
Db 661 EEKEIADFIDDPESPSTFNFQYPNOAFKRLHDLMHFTLNNDIVIKEMVESTIEYR 720
QY 721 QNPSRCSVSLSNVEARRFNKELSKP 749
Db 721 QNPSRCSVSLSNVEARRFNKELSKP 749

```

RESULT 2

B39898 cytosolic A2 (EC 3.1.1.4), cytosolic - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: B39898

R:Clark, J.D.; Lin, L.L.; Kriz, R.W.; Ramesha, C.S.; Sultzman, L.A.; Lin, A.Y.; Milona, Cell 65, 1043-1051, 1991

A:Title: A novel arachidonic acid-selective cytosolic PLA-2 contains a Ca(2+)-dependent

A:Reference number: A39898; MUID:9156305

A:Accession: B39898

A:Molecule type: mRNA

A:Residues: 1-749 <CLAS>

A:Cross-references: GB:M72394

C:Comment: This cytosolic phospholipase A2 translocates to membrane vesicles in response

C:Superfamily: cytosolic phospholipase A2

C:Keywords: calcium, carboxylic ester hydrolase; cytosol; inflammation

Query Match 95.5%; Score 3763; DB 1; Length 749;
Best local similarity 94.9%; Pred. No. 1,1e-266;
Matches 709; Conservative 24; Mismatches 14; Indels 0; Gaps 0;

```

QY 1 MSFIDYQHIIVEHOXSHKFTVVVLRATKVTKGAFGMDLTPDPVYELFISTTPDSKRT 60
Db 1 MSFIDYQHIIVEHOXSHKFTVVVLRATKVTKGAFGMDLTPDPVYELFISTTPDSKRT 60
QY 61 RHFNDINPWNTEFEFILDNPQENVEITLMDANYVMDTIGTATFTVSMKVGEKREY 120
Db 61 RHFNDINPWNTEFEFILDNPQENVEITLMDANYVMDTIGTATFTVSMKVGEKREY 120
QY 121 PEFNOVTEVMELEMSCPDLRFSMALCDQEKTFRQKRKEHIRESMKLLGPKNSG 180
Db 121 PEFNOVTEVMELEMSCPDLRFSMALCDQEKTFRQKRKEHIRESMKLLGPKNSG 180
QY 181 LHSARDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCAITYAGLSGTWMTLYSH 240
Db 181 LHSARDVPVVAIIIGSGGFRAMVFGSGVMKALYESGILDCAITYAGLSGTWMTLYSH 240
QY 241 PDFPEKGPEEINELMKNSHNPDLTLTPQKRYVESLTKKSSGQPVTFDIFGMLIG 300
Db 241 PDFPEKGPEEINELMKNSHNPDLTLTPQKRYVESLTKKSSGQPVTFDIFGMLIG 300
QY 301 ETLIHRMNTTSLSEKVTACPLPLFTCLHVKPDVSELMFADWVEFSPEIGMAKYG 360
Db 301 ETLIHRMNTTSLSEKVTACPLPLFTCLHVKPDVSELMFADWVEFSPEIGMAKYG 360
QY 361 TFMAPDLFGSKFPMGTIVVKKYEENPLHFLMGVGSASFILFNVLGVSQSOSRGSTMEBE 420
Db 361 TFMAPDLFGSKFPMGTIVVKKYEENPLHFLMGVGSASFILFNVLGVSQSOSRGSTMEBE 420
QY 421 LENITTKHIVSNDSSDDESHKPTENEDAGSDYQSDNQASWIRHMTALVSDSALFN 480
Db 421 LENITTKHIVSNDSSDDESHKPTENEDAGSDYQSDNQASWIRHMTALVSDSALFN 480
QY 481 TREGRAGKVNFMGLNLTSTPLSDPATQDSFDDDELDAVAADPDEFERIYEPDLY 540
Db 481 TREGRAGKVNFMGLNLTSTPLSDPATQDSFDDDELDAVAADPDEFERIYEPDLY 540
QY 541 KSKKIHVDSGLTFNLPYLLLRPQGVDLISFDSARPSSDPFKELLAEKAKKN 600
Db 541 KSKKIHVDSGLTFNLPYLLLRPQGVDLISFDSARPSSDPFKELLAEKAKKN 600
QY 601 KLPFPKIDYVDFREGIACGYFVKPNPDMKDCPTIIHFVLANINFRKXKAPGVRETE 660
Db 601 KLPFPKIDYVDFREGIACGYFVKPNPDMKDCPTIIHFVLANINFRKXKAPGVRETE 660
QY 661 EEKEIADFIDDPESPSTFNFQYPNOAFKRLHDLMHFTLNNDIVIKEMVESTIEYR 720
Db 661 EEKEIADFIDDPESPSTFNFQYPNOAFKRLHDLMHFTLNNDIVIKEMVESTIEYR 720
QY 721 QNPSRCSVSLSNVEARRFNKELSKP 747
Db 721 QNPSRCSVSLSNVEARRFNKELSKP 747

```

RESULT 3

I50699 cytosolic phospholipase A2 - chicken

C:Species: Gallus gallus (chicken)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: I50699

R:Nalefski, E.A.; Sultzman, L.A.; Martin, D.M.; Kriz, R.W.; Towler, P.S.; Knopf, J.L. J. Biol. Chem. 269, 18239-18249, 1994

A:Title: Delineation of two functionally distinct domains of cytosolic phospholipase

A:Reference number: A54908; MUID:94299545

A:Accession: I50699

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-748 <NLA>

A:Cross-references: EMBL:U010329; NID:g508624; PIDN:AAA53228.1; PID:g508625

C:Superfamily: cytosolic phospholipase A2
C:Keywords: cytosol

Query Match 86.0%; Score 3391; DB 1; Length 748;
Best Local Similarity 83.9%; Pred. No. 1,6e-239;
Matches 625; Conservative 64; Mismatches 56; Indels 0; Gaps 0;

QY 1 MSFIDPQHIIIEHSHKFTVAVLRATKTKGAFGMDLTPDPYVELFISTPDSRRKT 60
DB 1 MSFIDPQHIIIEHSHKFTVAVLRATKTKGAFGMDLTPDPYVELFISTPDSRRKT 60
QY 61 RHEFNDINPWNNEFETLDPNENVEITLMDANYDEFLGTATFVSSMKYGEKEV 120
DB 61 RHEFNDINPWNNEFETLDPNENVEITLMDANYDEFLGTATFVSSMKYGEKEV 120
QY 121 PFIRNOATEMLSEKLESCSDPLRFSMALCDDEKFRQOKNDIMOSKSFLEBENKN 180
DB 121 QLTNNVTENTLSEKLESCSDPLRFSMALCDDEKFRQOKNDIMOSKSFLEBENKN 180
QY 181 LHSADVPVVAIIIGSGGFRAMVGFSGVMKALYESGILDCATYVAGLSGTWYSTLYSH 240
DB 181 LHSADVPVVAIIIGSGGFRAMVGFSGVMKALYESGILDCATYVAGLSGTWYSTLYSH 240
QY 241 PDPEKPEEINELAKNVSNPLLLTPQKRVKRYVESLKKKSSGQPVFTDIFGMLIG 300
DB 241 PDPEKPEEINELAKNVSNPLLLTPQKRVKRYVESLKKKSSGQPVFTDIFGMLIG 300
QY 301 ETLHNHNTLSSIKKRVNTAOCPLPFTCLHVKPDVSELMFADWVEFSYEIGMAKYG 360
DB 301 ETLHNHNTLSSIKKRVNTAOCPLPFTCLHVKPDVSELMFADWVEFSYEIGMAKYG 360
QY 361 TFMAPDLFGSKFEMGTAVKYEENPLHFLMGVGSASFILFNRYLGVSQSGRSTMBEE 420
DB 361 TFMAPDLFGSKFEMGTAVKYEENPLHFLMGVGSASFILFNRYLGVSQSGRSTMBEE 420
QY 421 LENTTHIYVNDSDSDSHPEKGTENEDAGSDYOSDNOASWIRHIMAVSDSALFN 480
DB 421 LENTTHIYVNDSDSDSHPEKGTENEDAGSDYOSDNOASWIRHIMAVSDSALFN 480
QY 481 TREGRACKVHNFMLGLNNTSYPLSPDFAFODSDDELDAVADDEERIEYEPDLY 540
DB 481 TREGRACKVHNFMLGLNNTSYPLSPDFAFODSDDELDAVADDEERIEYEPDLY 540
QY 541 KSKRIHVDSGLTFENLPYPLLRQRCVDLIISFDSARPSDSSPPFEKELLAEKMAKN 600
DB 541 KSKRIHVDSGLTFENLPYPLLRQRCVDLIISFDSARPSDSSPPFEKELLAEKMAKN 600
QY 601 KLPPKIDPVPYFDEGLKECYVFKPKNDMEKDCPTIIHFVLANINFRKYAPGVPRETE 660
DB 601 KLPPKIDPVPYFDEGLKECYVFKPKNDMEKDCPTIIHFVLANINFRKYAPGVPRETE 660
QY 661 EEKFIADFIDDPESPFPNFQYPNQAFKRLDLMHFNLTNIDVYKEMAVESIEYR 720
DB 661 EEKFIADFIDDPESPFPNFQYPNQAFKRLDLMHFNLTNIDVYKEMAVESIEYR 720
QY 721 QNPSRCSVSLNVEARFENKELSL 745
DB 721 ENPSRCSVSLNVEARFENKELSL 745

RESULT 4

B54908
Phospholipase A2 cytosolic - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 07-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 31-Oct-1997
C:Accession: B54908
R:Meleleski, E.A.; Sultzman, L.A.; Martin, D.M.; Kriz, R.W.; Towler, P.S.; Knopf, J.L.;
J. Biol. Chem. 269, 18239-18249, 1994
A:Title: Delineation of two functionally distinct domains of cytosolic phospholipase A2;
A:Accession: B54908; MUID:94239545
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-741 <NBL2>
A:Cross-references: EMBL:U0329
C:Superfamily: cytosolic phospholipase A2

Query Match 70.8%; Score 2791; DB 2; Length 741;
Best Local Similarity 72.7%; Pred. No. 1.1e-195;
Matches 537; Conservative 81; Mismatches 111; Indels 10; Gaps 7;

QY 9 HIIEHSHKFTVAVLRATKTKGAFGMDLTPDPYVELFISTPDSRRKRRFNNDIN 68
DB 3 NIIEHSHKFTVAVLRATKTKGAFGMDLTPDPYVELFISTPDSRRKRRFNNDIN 62
QY 69 PVNNEFEFLDPNENVEITLMDANYDEFLGTATFVSSMKYGEKEVPIFNQVT 128
DB 69 PVNNEFEFLDPNENVEITLMDANYDEFLGTATFVSSMKYGEKEVPIFNQVT 122
QY 129 EMVLEMSLEVCSDPLRFSMALCDDEKFRQOKNDIMOSKSFLEBENKN 187
DB 123 KVFLLILEVCASDPLRFSMALCDDEKFRQOKNDIMOSKSFLEBENKN 182
QY 188 PVVAIIIGSGGFRAMVGFSGVMKALYESGILDCATYVAGLSGTWYSTLYSHDPEPK 247
DB 183 PVAIIIGSGGFRAMVGFSGVMKALYESGILDCATYVAGLSGTWYSTLYSHDPEPK 242
QY 248 PEEINELAKNVSNPLLLTPQKRVKRYVESLKKKSSGQPVFTDIFGMLIGTLHNR 307
DB 243 PGDINKELAKNVSNPLLLTPQKRVKRYVESLKKKSSGQPVFTDIFGMLIGTLHNR 302
QY 303 NIKLSLKGKINIGQSPPLPFTCLHVKPDVSELMFADWVEFSYEIGMAKYGTFMSPGL 362
DB 308 MNTLLSIKRVNTAOCPLPFTCLHVKPDVSELMFADWVEFSYEIGMAKYGTFMADL 367
QY 368 FGSKEFMGTAVKYEENPLHFLMGVGSASFILFNRYLGVSQSGRSTMBEELNTTK 427
DB 363 FGSKEFMGTAVKYEENPLHFLMGVGSASFILFNRYLGVSQSGRSTMBEELNTTK 421
QY 428 HIVNDSDSDESHPEKGTENEDAGSDYOSDNOASWIRHIMAVSDSALFN 487
DB 422 HIVNDSDSDESHPEKGTENEDAGSDYOSDNOASWIRHIMAVSDSALFN 480
QY 481 KVNHFMLGLNNTSYPLSPDFAFODSDDELDAVADDEERIEYEPDLYVSKRIHV 538
DB 488 KVNHFMLGLNNTSYPLSPDFAFODSDDELDAVADDEERIEYEPDLYVSKRIHV 547
QY 548 VDSGLTFENLPYPLLRQRCVDLIISFDSARPSDSSPPFEKELLAEKMAKNLPPPKI 607
DB 539 VDSGLTFENLPYPLLRQRCVDLIISFDSARPSDSSPPFEKELLAEKMAKNLPPPKI 598
QY 608 DPYFDEGLKECYVFKPKNDMEKDCPTIIHFVLANINFRKYAPGVPRETEKEETAD 667
DB 599 DSKYFDEGLKECYVFKPKNDMEKDCPTIIHFVLANINFRKYAPGVPRETEKEETAD 656
QY 668 FDIIDDPESPFPNFQYPNQAFKRLDLMHFNLTNIDVYKEMAVESIEYRONPSRCS 727
DB 657 FDIIDDPESPFPNFQYPNQAFKRLDLMHFNLTNIDVYKEMAVESIEYRONPSRCS 716
QY 728 VSLNVEARFENKELSL 746
DB 717 VSLNVEARFENKELSL 732

RESULT 5

T13162
cytosolic phospholipase A2 gamma - human
N:Alternate names: protein DKFZp586C0423.1
C:Species: Homo sapiens (man)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13162; T08799
R:Pickard, R.T.; Striffler, B.A.; Kramer, R.M.; Sharp, J.D.
J. Biol. Chem. 274, 8823-8831, 1999
A:Title: Molecular cloning of two new human paralogs of 85-kDa cytosolic phospholipase

A:Reference number: 217618; MUID:99185108
 A:Accession: T13162
 A:Status: preliminary; translated from GB/EMBL/DDJ
 A:Molecule type: mRNA
 A:Residues: 1-541 <PIC>
 A:Cross-references: EMBL:AF065214; NID:93811344; PID:93811345; PIDN:AAC78835.1
 R:Ansgorge, W.; Winkler, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: 216472
 A:Accession: T08799
 A:Molecule type: mRNA
 A:Residues: 443-541 <ANS>
 A:Cross-references: EMBL:AL050193
 A:Experimental source: adult uterus; clone DKEZ586C0423
 C:Genetics:
 A:Gene: cPLA2 gamma
 A:Map position: 19
 A:Note: DKEZ586C0423.1

Query Match 12.5%; Score 494.5; DB 2; Length 541;
 Best Local Similarity 26.8%; Pred. No. 3.6e-28;
 Matches 199; Conservative 88; Mismatches 190; Indels 129; Gaps 20;

135 SLEVCSCPDLFMSALCDDEKTRQQRKEHIRESMKKLLGPKNSEGLHSARDVPVVAIIIG 194
 3 SSEVSIIPGLQ-----KEEKAVERRRRLHVLAALKKL-----RIEADPAVVAIVIG 48
 195 SGGGFRAMGFSGVMAKALYESGILDCATYVAGSGSTWYSTIXSHDPFEKPEELINEE 254
 49 SGGGLRAHACLGVLSEMEQGLDAVYTAGVSGSTWAISSLYTN-----DDDMELAE 103
 255 LAMNVAHNPILLTLPQKVRKVESLWKKSSGQPV-----TFDIDGMLIGETLIH 305
 104 DLKH-----RFTQREMDLAKSLQKTYOARSEMYSLTDFAYAVYISKQTR 148
 306 NRMNTLSLIERKVNTAQCPPLPTCL--HVKPDVSELMEAD--WVESPYEIGMAKYYGP 362
 149 ELPEHSLHSMKKRVEEGTLPRPIFAIDNDLQPSMOEARAPETWFEPTPHHAGFPALGAF 208
 363 MAPDLGSKFEMGTVYKKVEENLHFLMGWGSAPSLFRVYGSGSGSGST-----416
 209 VSTTHGSKFKKRLVTRHERDLTFLRLGWSAL-----GNTVEYIREY 252
 417 MEELENITTKH-----VSNDSS-----DSDESHPEKGTENEDAGSYQSD 459
 253 IFQQLNLTIGKMRRAVANAISGHLIPARLRLQESSGGEHPP-----EDGG-----GE 304
 460 NQASWIRMI-----MALVSDSALFNTREGRAKVNHFMLGLNLTSTPLSLDFEATOD 514
 305 PEHTWLEMLENTPTSLKQEQHEDPE--RKGSLSNLM-----DEVKKT 348
 515 SFDDDELDAVADPDEER--IYEPIDVSKKIHVYDSGLTFNLPPLIRPGRVDLI 572
 349 GICASKWEGTTHNPLYKKGIDKIMSSKHLALVDAGLAINTPPPLVLPPTREHLLI 408
 573 SFDFSARPSDSPFKELLAEKMAKMKLPPFKIDPYVED--REGUKCEYVFKPKNPD 630
 409 SFDFS-----GDFETIARTTYCRRHKIPFQVEAEALDLMASKAPASCIILKGTG--461
 631 EKDCPTIIHFVLANIN 646
 462 ----PVVMHPELFENID 473

RESULT 6
 S29318
 lysophospholipase (EC 3.1.1.5) precursor [validated] - Penicillium notatum (fragment)
 C:Species: Penicillium notatum
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 19-Jan-2001
 C:Accession: S29318; S39881; S22045
 R:Masuda, N.; Kitamura, N.; Saito, K.
 Eur. J. Biochem. 202, 783-787, 1991

A>Title: Primary structure of protein moiety of Penicillium notatum phospholipase B d
 A:Reference number: S29318; MUID:92111525
 A:Accession: S29318
 A:Molecule type: mRNA
 A:Residues: 1-612 <MAL>
 A:Cross-references: EMBL:X60348; NID:93183; PIDN:CAA2906.1; PID:93184
 A:Accession: S39881
 A:Molecule type: protein
 A:Residues: 10-20;185-199 <MA2>
 C:Superfamily: yeast lysophospholipase
 C:Keywords: carboxylic ester hydrolase; glycoprotein
 F:1-9/Domain: signal sequence (fragment) #status predicted <SIG>
 F:10-612/Product: lysophospholipase #status experimental <MAT>
 F:41,81,116,223,267,306,335,427,440,446,477,498,526,532,567,571/Binding site: carboxy

Query Match 5.6%; Score 221.5; DB 2; Length 612;
 Best Local Similarity 22.6%; Pred. No. 3.8e-08;
 Matches 112; Conservative 78; Mismatches 145; Indels 161; Gaps 24;

140 SCPDLRFSMALDQEKTRQQRKEHIRESMKKLLG-----PKNSRGLHSARD 186
 28 SRPTVSAAKLSTNYSWLEVRGKTLALDKDFGHVKKYGDYVGLDKHS---GNSS 84
 187 VPVVAIIIGSGGFRAMGFSGVMAKAL-----YESGILDCATYVAGSGSTWYMS 235
 85 LPIGIVAGSGGFRALMNGAVKAFDSRDNATATGHLGGLQASATYISGLSGSWLIG 144
 236 TLVSHDPFE-----KPEELINEELKMNVAHNPILLTLPQKVRK 275
 145 SIYIN-NFTTVDKLQTHAGSVWQFGNSIIEGPDAGIOLLDSAGY-----YKDL 193
 276 VESIMKSSGQGVPTFDIFGMLIGETLI--HNRNNTLSLKE--KYNTAQCPPLPT 330
 194 ADVVDKRAKAGFTTITDWRALSYQMRNASGGLSTYWSIADTPPEQDDYPPFV 253
 331 CLAVKPDVSELMF--ADVVESPYEIGMAKYYGTMAPDLFGSKFPMGVVKKYENPLH 387
 254 ADGRNP--GELVIGNSJTYEFENPWE-----FCTF-DPTIFG--FV-----PLE 292
 388 FLMGWGSAPSLFNFVYLGVSQSGSTMEELNITTKHIVSNDSSDSDESHPEKOT 447
 293 YL-----GSKFEGGSLP-----SNMSCIRGDS-----315
 448 ENEDAGSDYQSDNQASWIRMIHALVSDSALFNTREGRAKVNHFMLGLNLTSTPL 507
 316 ----AG-----FVIGTSSLEN-----QFLQTN-TTSLP-SFI 343
 508 SDFATQDSFDD--ELDAVADPDEFEIYEPDL--VSKKIHVYDSGLT-FNLPPPLI 562
 344 KQVFNGLTFLDLKSDNDIASYDNPYKYNHSSPYAAQKLDVVDGEGDQVPLHPLI 403
 563 RPRGVDLIISDFSA 578
 404 QPERHVDVIFAVDSSA 419

RESULT 7
 S53037
 PLB1 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YH8270.10c; protein YKR008c
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999
 C:Accession: S53037; A53647
 R:Devlin, K.; Churcher, C.M.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53037
 A:Molecule type: DNA
 A:Residues: 1-664 <DEV>
 A:Cross-references: EMBL:Z48613; NID:9728645; PIDN:CAA88523.1; PID:9728655; MIPS:TMRO
 A:Experimental source: strain Ab972
 R:Lee, K.S.; Patton, J.L.; Fido, M.; Hines, L.K.; Kohlwein, S.D.; Paltauf, F.; Henry,

submitted to the EMBL Data Library, March 1995

A:Reference number: S53028

A:Accession: S53035

A:Molecule type: DNA

A:Residues: 1-706 <DEV>

A:Cross-references: EMBL:Z48613, NID:g728645; PIDN:CAA8521.1; PID:g728653; GSPDB:GN0001

A:Experimental source: strain AB972

C:Genetics:

A:Gene: MIPS:YMR006c; PLB2

A:Map position: 13R

C:Superfamily: yeast lysophospholipase

C:Keywords: carboxylic ester hydrolase; glycoprotein; transmembrane protein

F:690-706/Domain: transmembrane #status predicted <TM>

Query Match 5.3%; Score 207.5; DB 2; Length 706;
Best Local Similarity 21.1%; Pred. No. 5.1e-07;
Matches 118; Conservative 100; Mismatches 195; Indels 147; Gaps 28;

```

QY 138 VCSGPD-----LRFSGALCDOEKTRFQORKEHRESMKLLPKNK-----EGHSA 184
DB 34 IIPCSDDTSLVRNMSGSTATDMLKRDATYKELHSFLSRATSNESDSTLSLTFSS 93
QY 185 R--DPPVVAIIISGGGFRAMVGFSGVMKALY-----SGILDCATYVAGLSGSTM 232
DB 94 NSSNPVKIISAGSGGGRYMLGAGAGIAMDNRTDGNHGLGILQSTYLSGLSGMW 153
QY 233 YKSTL-YSHHPPEKPEPEINE-ELMKNVSH--NP---LLILLTPQKRYVESLKKKS 284
DB 154 LMGTLAMNMTSVQELVDHMSSEDSIMNTKSIYVNGSGNLTYTEIRMESIVQEOAKSD 213
QY 285 SCQPTFTDFGMLIGETLIHNRMT---TLSSLK--EKVMTACQPLFLFCLHKKRPV 338
DB 214 AGFNISLSLDMARALSYNFFSLPDGSLTWSLSLDVDFKNNGEMPLFIYVADGRYPET 273
QY 339 SEL-MFADWVEESPYEIGMAKYGTFMADPLFGSKFFMTGVVKKYEENPLHFLMGVGSNAF 397
DB 274 TVININATLFEETPE-----NVTNGKRPVKNDCVS-----GYDN--AG-- 329
QY 398 SLTFN-RVLGSGSGSGSTMEELNITTKHIVSNDSDSDSEHPEKGTENEDAGSY 456
DB 298 NAFETVKKYLG-----NVTNGKRPVKNDCVS-----GYDN--AG-- 329
QY 457 QSDNQASMIHIMALVSDALENTREGRAKGVHNFMLGLNLTSPPLSLDFPATOD-- 514
DB 330 -----FYATISASLFN-----EESLEASTSTYTKM--INSPANKIYN 364
QY 515 --SPDDELDAAVADP--DEF-ERIEPLDVSKKIHVDSGLT-FNLPLPLILRPORG 567
DB 365 NISQDDDDAIYAANPFKTEFVDNRVYTSIYDADDLFLVDGGEQDQNLPLVLKKERD 424
QY 568 VLLIISFDSAPRSDSP--FKELLIAEKAKMKK-LPFRPI-DPIYVDRGGLKECYAF 623
DB 423 LDVVFALDLSIDTDSWPSGVCMTYTERQYSKQGGKMGAPYVPDVTFLNLGLTNKPTF 484
QY 624 ---KPKN-PDMKDCPTIIF 639
DB 485 FGCDAKNLDELFIPIPLVY 504

```

RESULT 10

S66693

hypothetical protein YOL011w - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein O2349

C:Species: *Saccharomyces cerevisiae*

C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000

C:Accession: S66693

R:Hughes, B.; Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66685

A:Accession: S66693

A:Molecule type: DNA

A:Residues: 1-686 <HUG>
A:Cross-references: EMBL:Z47453, NID:g1419780; PIDN:CAA99010.1; PID:g1419781; GSPDB:G
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MIPS:YOL011w
A:Map position: 15L
C:Superfamily: yeast lysophospholipase

Query Match 5.2%; Score 205.5; DB 2; Length 686;
Best Local Similarity 22.2%; Pred. No. 6.8e-07;
Matches 139; Conservative 99; Mismatches 186; Indels 203; Gaps 38;

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QY 140 SCPP-----LRFSGALCDOEKTRFQORKE-----HRESMKLLGPKN 177
DB 39 SCPPDINLVREATSIQNSANLEKRNKYTSVALDELFRATANSDESSEVLSKFLPFGN 98
QY 178 SEGHSARDVPVAIIISGGGFRAMVGFSGVMKAL-----YE--SGILDCATYVAGL 227
DB 99 SENL-----PKIYAVSGGGRYMLTGAGVLAADNRTEGAYEHGLGILQSTYLSGA 152
QY 228 SGSTYMTSLYSHPPPEKPEPEIN-----ELMKNVSHNPL-----LLTP-----Q 270
DB 153 SCGNMLVGTL-----ALNNMTSVODILNNMONDSDIMDLSDSIYPPGINIEK 200
QY 271 KYKRY-----VESLKKKSGQPTFTDFGMLIG---ETLIHNRMTTSLSEKYN 320
DB 201 TAKRNDHISNAVES---KONADYNTSLADIMGRALALYFPLNNGGIGLTYSSIRD--- 254
QY 321 TACQPLPLETCLHVRDVSSELMFADWVEESPYEIGMAKYGTFMADPLFGSKFF-MGYVK 379
DB 255 -----FPVF-----QNAEMPF-----PISVADGRYP-----GTVININATV- 286
QY 380 KYEENPLHFLMGVGSAPSILFN-RVLGSGSGSGSTMEELNITTKHIVSNDSSDSD 438
DB 287 -FEFNP--FEMSGMPSLNSFANVYLG--NVSNGVPLE----- 321
QY 439 DESHEPKGTENDAGSDYQSDNQASMIHIMALVSDALENTREGRAKGVHNFMLGLN 498
DB 322 ---RGKCT---AGFD-----NAGFI-----MGTSTLTFN-----QFLLRIN- 351
QY 499 NTSYP--LSPISDFATQDSFDDDELDAVADDER-----ERIEPLDVSKKIHVDS 550
DB 352 STLPSFIFRLAHFLKD--LSQDFNDIAVYSPNPKDKFLDSDTTYSIVSDSLFLVDG 410
QY 551 GL-TFNLPYPLLRORGVDLISFDSARPSSDPKELL--LAEKAKMKK-LPFRK 606
DB 411 GEDDERVPLPLIQERVDLIFAVDNSADMRLAMPDGSLLVHYERQYVKGQGSSEFY 470
QY 607 I-DPVVFDRGGLKECYVFP-----KNPDMKDCPTIIFVLINIFRKYKAPGVP 657
DB 471 VPDNTMTFVNLGLK-----KPFEGGDANNLIDQLYIPLVYLPLNAEVSFNSNGAFKLS 526
QY 658 ETEEEK-----EIADFIF-DDPE 675
DB 527 YSESORSMWQNGFEIATRNFTDDPE 553

```

RESULT 11

T40991

probable lysophospholipase precursor - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C:Accession: T40991

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Voiclaert, G.

submitted to the EMBL Data Library, March 1999

A:Reference number: Z21962

A:Accession: T40991

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-623 <LYN>

A:Cross-references: EMBL:AL049559; PIDN:CA840176.1; GSPDB:GN00066; SPDB:SPCC1450.09c

A:Experimental source: strain 972h-; cosmid c1450

C:Genetics:
A:Gene: SPDB:SPC1450.09c
A:Map position: 3
C:Superfamily: Yeast Lysophospholipase

Query Match 4.9%; Score 194.5; DB 2; Length 623;
Best Local Similarity 20.7%; Pred. No. 3.7e-06;
Matches 102; Conservative 70; Mismatches 174; Indels 147; Gaps 19;

QY 140 SCDD---LR-FSMALCDDKTFPQCKEHRRESMKLL---GPK-NSEGHSARDVPYVA 191
DB 67 ACPGSGLLRPASDGLSTGQEFYDKRVKYNKSLSFISKYTKGLDKTQSVLNTDTPRLG 126
QY 192 IIGSGGGFRAMVGFSGVMKALYE-----SGILDCATYVAGLSGSTMVSTL----- 237
DB 127 IAISSGGFAMLTGAGAINAPDARNNGNTSLGSIILQSSMYLIGLSGSMVGVSAVANNFA 186
QY 238 ---YSHPDFPEKGPPEINEELMKNVSHNPLLLTPQK-----VKRYVESLMKKSSG 286
DB 187 NTFPLHDD-----VWNLDS---LFAPYDAFENFYIYQEWFEQYLQKKNAG 230
QY 287 QPTEFDIDGMLIGETLIH---NRMTTSLSEKRY--NTAQCPPLFTCLHVKPDVSEL 341
DB 231 FNVSTIDLMGRALAKLVNPLTGCANTFTSSVNTETWFOGDEFPPIIADNIEGETVI 290
QY 342 MFADWY-EFSPYEIGMAKYG--TFNAPDLFGSKFEMG-----TVKKYEENPLHPLMGVW 393
DB 291 PLNDYFEETPIEFQWMDGVSEFIMEYTGTLINGIPLNESCYNFND--AGFLMGIS 348
QY 394 GSAFSLIFNRVLGVSGSGRSGTMEELENTTKHIVSNDSDSDSEHPKGTENEDAG 453
DB 349 SNVFS-----GILPATNASLTSANNFTNNAVLSFLEMAEDQLDVGLYP----- 392
QY 454 SDYQSDNQASWTHRMIMALVSDALFNTREGRAGKYHNFMLGLNMTVPSPLSDPANTQ 513
DB 393 NPYQCGNMS-----NTTTNLEPYPIIEELI 419
QY 514 DSFDDELDAVAADPEFERIYERPLDYKSKIHVDSGLTFNLPYPLIRPQGVDLIS 573
DB 420 DGGSDSE-----GTFPMPPLHQPQDVYIFA 445
QY 574 PFDSARPSDSSPP 586
DB 446 IDGGYQASATSGWP 458

RESULT 12
T38006
Probable lysophospholipase precursor - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T38006
R:Churcher, C.M.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21761
A:Accession: T38006
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-624 <CHD>
A:Cross-references: EMBL:Z9958; PIDN:CAB16353.1; GSPDB:GN00066; SPDB:SPAC1A6.03c
A:Experimental source: strain 972h-; cosmid c1A6
C:Genetics:
A:Gene: SPDB:SPAC1A6.03c
A:Map position: 1
C:Superfamily: Yeast Lysophospholipase

Query Match 4.9%; Score 192.5; DB 2; Length 624;
Best Local Similarity 20.7%; Pred. No. 5.2e-06;
Matches 139; Conservative 97; Mismatches 226; Indels 209; Gaps 34;
QY 140 SCDD---LR-FSMALCDDKTFPQCKEHRRESMKLLGPKNSEGLH-----SARDVP 188

DB 38 TCPSPDMLRPASDGLSGEQSFEIDKRIPIKINTQMSFI---SNTGLDVVNSYINSDGP 94
QY 189 VYAILGSGGFRAMVGFSGVMKALYE-----SGILDCATYVAGLSGSTMVSTL----- 237
DB 95 RUGLAFSGGGLRAMVGGVLTNAPDSRNGSSSLAGLSAMTLAGLSGSMVGVSAVANNFA 154
QY 238 ---YSHPDFPEKGPPEINEELMKNVSHNPLLLTPQKRYVESLMKK 283
DB 155 NFANITYLNDNVNMLHSHVAFAPHG-----DNVEENLAYDDL-----DDELQKK 199
QY 284 SSGQPYTFDIDGMLIGETLI---HNRMTTSLSEKRY--NTAQCPPLFTCLHVKPDV 338
DB 200 DAGFDSTIDLMGRALSRLKVDATOGCPNFTFSINQNTFOQVADYPPYPI-----I 251
QY 339 SELMFAD-----WVESPYEIGMAKYG--TFNAPDLFGSKFPMGT-----VKRYE 382
DB 252 SDSRLBEKKAIPANTSIFFETPIEFQWMDGIAFLPMETVGHILKNVPPDHKCIKRTD 311
QY 383 ENPLHFLMGVWSAFSILFNRYLVGSQSQRSGTMEELENTTKHIVSNDSDSDSEH 442
DB 312 N--AGFVWG---TSATLFTFTPL-LEMSQ-----EVTNSNLTLDI----- 344
QY 443 EPKGTENEDAGSDYQSDNQASWTHRMIMALVSDALFNTREGRAGKYHNFMLGLNNTSY 502
DB 345 -----IHKYFEKLSQDQ-----NDIAPY 362
QY 503 PLSPDLPATQDSFDDELDAVAADPEFERIYERPLDYKSKIHVDSGL-TFNLPYPLI 561
DB 363 P-NPYQFTTNT-----TVKNP--FER-FDTID-----LVGGGDDENITWPL 403
QY 562 LRPQGVDLIISPFARSDDSSPPKELLAEK---WAKMKNLPPPKIDPYVFDREGIK 618
DB 404 LHPQRFYDVFAVDATYDSDNGMPDSSIVTYERITTYNANKSVYGRPPYIPDD-- 460
QY 619 ECVYFKPKNDMEKCPPTIHFYLANINFRKYYKAPGVPRTEEEKELADPIDDPSPP 678
DB 461 -----TTISLGL-NTHPFFGCDG--RNT-----TAGNHTVDNNTPL 495
QY 679 STEFQYPONAFKRLDLMHFTLNINIDVYKEMVE--STEYRQNPSSRCSYLSNVEAR 726
DB 496 LYY---FPNTPWYYSNISIF-TMSANDTSSGILEMAALSTATONNSDSRAVCLACAMIO 551
QY 737 RFENKEFLSKP 747
DB 552 RSLERKKNMSTP 562

RESULT 13
T51799
C1B1-like protein - Arabidopsis thaliana.
N:Alternate names: protein T5K6_90
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51799
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.D.; Voet, M.; Robben, J.; Volckaert, G.;
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25455
A:Accession: T51799
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-574 <BEV>
A:Cross-references: EMBL:AL391222
A:Experimental source: cultivar Columbia; BAC clone T5K6
C:Genetics:
A:Map position: 5
A:Introns: 35/3; 77/3; 94/3; 135/1; 177/3; 211/3; 236/3; 263/2; 313/3; 390/3
A:Note: T5K6_90

Query Match 4.5%; Score 178.5; DB 2; Length 574;
Best Local Similarity 22.1%; Pred. No. 4.8e-05;
Matches 71; Conservative 58; Mismatches 127; Indels 65; Gaps 12;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2001, 16:29:13 ; Search time 13.89 Seconds
(without alignments)
1110.307 Million cell updates/sec

Title: US-09-250-083A-2

Perfect score: 3942
Sequence: 1 MSFIDPYQHIVHEQYSHKF.....LSNVEARRFENKEFLSRPKA 749

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3942	100.0	749	1	US-08-046-508-2
2	724	18.4	913	3	US-08-827-208-3
3	724	18.4	913	4	US-09-500-358-3
4	724	18.4	913	4	US-09-498-809-3
5	499.5	12.7	541	3	US-08-890-615-2
6	494.5	12.5	541	3	US-09-045-185-2
7	232.5	5.9	649	3	US-09-295-186-18
8	221.5	5.6	612	3	US-09-295-186-16
9	219.5	5.6	664	3	US-09-295-186-17
10	201.5	5.1	573	3	US-09-295-186-11
11	200.5	5.1	552	3	US-09-295-186-11
12	112	2.8	140	2	US-08-609-049A-16
13	108	2.7	897	1	US-08-095-737-4
14	108	2.7	897	1	US-08-480-145-4
15	108	2.7	897	2	US-08-477-389-4
16	107	2.7	688	1	US-08-221-817-19
17	107	2.7	688	1	US-08-454-439-19
18	107	2.7	688	5	PCT-US94-10487-19
19	103.5	2.6	896	1	US-08-471-251A-2
20	103	2.6	896	1	US-08-095-737-2
21	103	2.6	896	1	US-08-480-145-2
22	103	2.6	896	2	US-08-477-389-2
23	103	2.6	3418	2	US-08-639-501-2
24	103	2.6	3418	3	US-09-044-946-2
25	103	2.6	3418	3	US-08-755-587-44
26	103	2.6	3418	3	US-09-044-908-2
27	102	2.6	3418	2	US-08-603-7530-4

28	102	2.6	3418	4	US-09-099-753-4	Sequence 4, App11
29	102	2.6	3418	4	US-08-986-106-4	Sequence 4, App11
30	101.5	2.6	854	2	US-09-070-060-4	Sequence 4, App11
31	101.5	2.6	854	3	US-09-357-746-4	Sequence 4, App11
32	101	2.6	2938	5	PCT-US94-00198-3	Sequence 3, App11
33	100.5	2.5	873	3	US-09-187-331-6	Sequence 6, App11
34	100.5	2.5	911	3	US-09-356-952-6	Sequence 6, App11
35	100.5	2.5	911	3	US-08-392-946-1	Sequence 1, App11
36	100.5	2.5	925	2	US-08-504-169-1	Sequence 1, App11
37	100.5	2.5	925	2	PCT-US94-14893-1	Sequence 1, App11
38	100.5	2.5	925	5	US-08-242-932-2	Sequence 2, App11
39	100	2.5	984	1	US-08-714-481-2	Sequence 2, App11
40	100	2.5	984	1	US-08-714-481-2	Sequence 2, App11
41	100	2.5	984	5	5266464-2	Sequence 2, App11
42	99.5	2.5	671	6	5266464-2	Sequence 10, App1
43	97	2.5	2366	1	US-08-480-604A-10	Sequence 10, App1
44	97	2.5	2366	2	US-08-405-496A-10	Sequence 10, App1
45	96.5	2.4	904	4	US-08-632-537-1	Sequence 1, App11

ALIGNMENTS

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RESULT 1
US-08-046-508-2
; Sequence 2, Application US/08046508
; Patent No. 5328842
; GENERAL INFORMATION:
; APPLICANT: CHOU et al.
; TITLE OF INVENTION: COMPOUNDS, VECTORS AND METHODS FOR
; NUMBER OF INVENTION: EXPRESSING HUMAN CYTOSOLIC PHOSPHOLIPASE A2
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Patent Division/RSM
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,508
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph A. Jones
; REGISTRATION NUMBER: 26,472
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-5183
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 749 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-046-508-2

Query Match      100.0%; Score 3942; DB 1; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MSFIDPYQHIVHEQYSHKFTVVVLRATKYTGAFGMDLTPPPYELFISTPDSRRKT 60
DB      1 MSFIDPYQHIVHEQYSHKFTVVVLRATKYTGAFGMDLTPPPYELFISTPDSRRKT 60
OY      61 RHFNNNDINPYWNETFEFIDDPNCENVLEITLMDANYVMDETLGTATFTVYSKMGKEK 120
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Db 61 RHFNNDINPNMTEFEFLIDPNOENVLEITLMDANYMDETIGTATFTVSSMKVGEKREY 120
QY 121 PRIFNVQVTEVMELEMSLEVCSCPDLRFSMALCQDEKFRQORKEHRESKAKLLGPNNSG 180
Db 121 PRIFNVQVTEVMELEMSLEVCSCPDLRFSMALCQDEKFRQORKEHRESKAKLLGPNNSG 180
QY 181 LHSARDVPVVALIGSGGGRAMVFGVAKALYESGILDCATYVAGLSSTWYMTLYSH 240
Db 181 LHSARDVPVVALIGSGGGRAMVFGVAKALYESGILDCATYVAGLSSTWYMTLYSH 240
QY 241 PDPPEKGEPEINDELKKNVSHNPDLILTPQKRYVESLTKKSSGQPYTFDIFGMLIG 300
Db 241 PDPPEKGEPEINDELKKNVSHNPDLILTPQKRYVESLTKKSSGQPYTFDIFGMLIG 300
QY 301 ETLIHRMTTSLSKKNTAOCPLFTCLHVKPDVSELPMADVESPVEIGAKKG 360
Db 301 ETLIHRMTTSLSKKNTAOCPLFTCLHVKPDVSELPMADVESPVEIGAKKG 360
QY 361 TEMAPDLFGSKFFMGTVVKKYEENPLHFLMGVGSASFILFNVLGSGSGSGSTMEBE 420
Db 361 TEMAPDLFGSKFFMGTVVKKYEENPLHFLMGVGSASFILFNVLGSGSGSGSTMEBE 420
QY 421 LENITTKHIVSNDSDSDSHBPKGTENEDAGSDYQSDNQASWIRHMTALVSDALFN 480
Db 421 LENITTKHIVSNDSDSDSHBPKGTENEDAGSDYQSDNQASWIRHMTALVSDALFN 480
QY 481 TREGRAGKHNMFLGNTLNTSYPLSLDPAFQDSDFDDELAAVADPDEFERIYELPV 540
Db 481 TREGRAGKHNMFLGNTLNTSYPLSLDPAFQDSDFDDELAAVADPDEFERIYELPV 540
QY 541 KSKKIHVDSGLTFNLPYLILRPOGVDLISFDSARPSSSPFEKLLAEKAKKN 600
Db 541 KSKKIHVDSGLTFNLPYLILRPOGVDLISFDSARPSSSPFEKLLAEKAKKN 600
QY 601 KLPFRIDYVDRGLKACCYFKPKNPMEKDCPTIHFVLANINFRKYKAPGVRETE 660
Db 601 KLPFRIDYVDRGLKACCYFKPKNPMEKDCPTIHFVLANINFRKYKAPGVRETE 660
QY 661 EEKEIADFIDDPESPSTFNFQYQNAFKRLHDMHFNLTINIDIVEKAMVESLEYR 720
Db 661 EEKEIADFIDDPESPSTFNFQYQNAFKRLHDMHFNLTINIDIVEKAMVESLEYR 720
QY 721 QNPSRCSVLSNVEARFENKEFLSKPKA 749
Db 721 QNPSRCSVLSNVEARFENKEFLSKPKA 749

```

RESULT 2
US-08-827-208-3
Sequence 3, Application US/08827208
Patent No. 6025178

GENERAL INFORMATION:

APPLICANT: Chlou, Xue-Chiou C.
APPLICANT: Kramer, Ruth M.
APPLICANT: Pickard, Richard T.
APPLICANT: Sharp, John D.
APPLICANT: Sciflier, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,208
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-827-208-3

Query Match
Best Local Similarity 24.8%; Score 724; DB 3; Length 913;
Matches 208; Conservative 152; Mismatches 268; Indels 210; Gaps 26;

QY 21 TVVILRATKVTGAFGMDLTPDPYVELEISTTPDSRRKTRHFNNDINPNMTEFEFLID 80
Db 145 TVRVLQAHRLPS---KDLVTPSDCYVTLMVLPACSHRLQTRFKVKNSSSVWMSQHFRIH 201
QY 81 PNOENVLEITLMDANYM-DELTGATFTVSSMKXGE-----KKEYPFE--- 122
Db 202 KOLKNVMEIKVFDQDLVGTDDPVLSVLPDAGFLRAGEFRRESFSLSPOGEGRLEVEFRLQ 261
QY 123 -----IFNOV-----TEMYL----- 132
Db 262 SLADNREMLVNSGVLVARELSCLHVQLEETGQKSEHRVQLVVGSGCPQASVGTGT 321
QY 133 -----EMLSEVSCPD----- 143
Db 322 FRFHCPACWEOELSTRLODAPPEOLKAPLSALPSCQVRLVPTSOEPLMRYELKEAGL 381
QY 144 ----LRFSMALDDEKTEFQORKEHRESKAKLLGPKNSEGLSHSARDVYVVALIGSGGE 199
Db 382 RELAVRVLGFGPAEBOATLSRKKOYVAAALROAL--OLDGLQDEDEIVYVAAIMATGGGI 438
QY 200 RAMVGFSGVMKALYESGILDCATYVAGLSGSTMWSTLYSHDPDPFK--GPEIINEELM 256
Db 439 RAMTSLYGQLAGLKEGLDLDVSYITGASGSTMALANLYEDEWESQKDLGPTL---LK 495
QY 257 KVVSHNPDLILTPQKRYVESLTKKSSGQPYTFDIFGMLIGETLLHNRMT--TLSL 315
Db 496 TQVTKKKGVLVAPSOLOARYOLASRARLGPSCPTNMA-LINALLHDEPHDKLSDQ 554
QY 316 KEKVNTAOCPLFLFNCILNKH-PDVSELPMADVESPVEYIGAKGTFPAPDLFGSKFFM 374
Db 555 REALSHGONPLTYCALNKKOSLTTFEEGENCEPSPEVGGPKGATLPSELFSSEFFM 614
QY 375 GTVAVKYEENPLHFLMGVGSASFILFNVLGSGSGSGSTMEBEL-----ENITTKH 428
Db 615 GGLMKRLPRESRICFLEGIKSNLYA-----ANLDOSLVWASRPSQFMRW 658
QY 429 IVSNDSSDSD-----ESHEPKGTENEDAGSDYQSDNQASWIRHMTALVSDALFNTEBG 484
Db 659 VANOANLDEKEQVPLKIEBPSTAGRIA--EFFTD-----LLTWRP 697
QY 485 RAGKXVHNFMLGNTLNTSYPLSLDPAFQDSDFDDELAAVADPDEFERIYELPVKSKK 544
Db 698 IAOATHNPLRGLHFKHDYFOHP--HFSTWKAATYLDGL-----LPSPSPH 742

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[illegible]

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Db 145 TVNLQAHRLPS---KDLVTPSDCVYVTLMLPTACSHRLQRTFVANKSSSSVWNGSFHRH 201
QY 81 PNOENVLEITLMDANYVA--DETCTATFVYSSMKVGE-----KKEVP---1222
Db 202 ROLKNVMEIKVFDOLVYTGDDPVLVLFDAGTLRAGEFRRESFSLSPQEGRLVEFRLO 261
QY 123 ---IFNOV-----TEMVL-----133
Db 262 SLADRGEMLVNSGVLVARELSCLHVOLEETGDKSSSEHRVOLVVGSGCEGPQEA SVGTGT 321
QY 133 -----EMSLVSCSDP-----143
Db 322 FRFHCPACWBEELSIRLADAPAEEDOLAPLSABSGVYVRLVFTPSQEPIMKVELKKEAGL 381
QY 144 ---LRFSMALCDEKTEFTROQRKEHIRESMKRLKPKNSBGLHSARDVPVVALIGSGGF 199
Db 382 RELAVRLGFGCAEEQAFLSRRKQVVAALROAL---QLDDQLDEDELPVAVIATGGGI 438
QY 200 RANVGFSSVMKALYESGLDCATYVAGISGSTMWMLYLSHPDPEK---GRELINELM 255
Db 439 RAMTSLVGQALGELGELLDVSYITGSGSTMALANLYEDPEMSOKDLAGPTEL---LK 495
QY 257 KNVSNPILLTLPCKVKRYVSLMKKKSSGQPVFTDIPGMLIGETPLIHNNMNT--TSSL 315
Db 496 TQVTKNKLGVLAPSOLOQLRBLERARLGLPSCFTNLMA--LIMEALLHDPDHKLSDO 554
QY 316 KEKVTAQCPRLPTFCTLHVK--PDVSELMFADWVEFSPYELIGMAKYGTGFMAPDLGSKFFM 374
Db 555 REALSHGONPLPYICALNTKQOSLTFTEFGMCEFSPEYEVGFPRYGAFAIPSELGSEFFM 614
QY 375 GTVYKKYEENPLRLMGVWSAFSILFNRYLVGVSOSRGSTMEEL-----ENITTKH 422
Db 615 GQMKRLPESRIKCELEGISWMLYA-----ANLDDSYLWASEPQFMDRW 656
QY 429 IVSNDDSSDD-----ESHEPKGTENEDAGSDYOSDQNASWHRIMALVYSALFNTREG 484
Db 659 VRNOANLDEKEVPLKIEEPSTGRTA--EFTD-----LITWRP 697
QY 485 RAGVHNEMELGINTSYPLSLSDFATQDSFDDDELDAVADPEDEFERIEPLDVSKK 544
Db 698 LAQATHNLRQLRHLHKQVFOHR--HFSTWKATITLDGL-----LTPSEPH 742
QY 545 IHVVDGSLTFMLPYPLILRPGVDLISDFSAKPSDSSPFKELLIAEKWAKMKLPLF 604
Db 743 ICLLDVGLINTSCPLRLQPRDVLILSIDYNLHGA-----FOOLOLGRFCOEOGIPF 797
QY 605 PKIPIYVDRBGLKECYFYK--PKNPDMEKDCPTIIHVLANINFRKKYKAPVRETEBEK 665
Db 798 PPLSPSEEDQPRCHTFSDPTCP---GAPVYLHFLVSDSPRESABPV--RTTPEA 852
QY 664 EIADFDIDDEPSEFSTFNPFOYQNAQFKRLHDLHFNLTNNIDVIEKAMVSEIYRQ 721
Db 853 AAGEFVNL--SSSDSPHYTKYTVSQEDVDKLLHLYHNVCNNQOBDLEALRQAVGRRQ 909

RESULT 4
US-09-498-809--3
Sequence 3, Application us/09498809
Patent No. 6242206
GENERAL INFORMATION:
APPLICANT: Chlou, Xue-Chlou C.
APPLICANT: Kramert, Ruth M.
APPLICANT: Rickard, Richard T.
APPLICANT: Sharp, John D.
APPLICANT: Stiffler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NOCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana

```

COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,809
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/827,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-498-809-3

Query Match 18.4%; Score 724; DB 4; Length 913;
Best Local Similarity 24.8%; Pred. No. 8,1e-58;
Matches 208; Conservative 152; Mismatches 268; Indels 210; Gaps 26;

21 TVVVLATVTVTGAFGMDLTPDPVYELFISTTPDSRRKTRHFNNDINPVNTEFEILD 80
145 TVAVLQAHRLPS---KDLVTPSDCVYTLMLPTCSHRLQTRVYKSSSVYMNQSFHRIH 201
81 PNEENVLETTMDANYVM-DELTGATFTVSSMKVGE-----KKEVFF---122
202 ROLKNVMEIKVEFDQDLVTDQDVLVFLDAGTLRAGEFRRESFSLSPGEGRLVEFRLO 261
123 -----IFNOV-----TEWVL-----132
262 SLADRGEMLVNGLVARELSCLHVLQLEETGDKSSEHRYQLVVPQSCGPQASVGTGT 321
133 -----EMSLVSCSPD-----143
322 FRHCPACWQELISRLQDAPEBQKAPLSALPSSGVNRLVFTPSQEPIMRVELKKEAGI 381
144 ----LFSNALDQDEKTFNQQRKEHRESMKKILGPKNSEGLHSADVNVVVALSGGGE 199
382 RELAVRLGGPCAEEQAFISRRQVVAALROAL---QDGDQDEDEIPVVAIMATGGGI 438
200 RAWVGSVWKALYEGSGLIDCATVYAGLSGTFWYNSTLYSHDPPEK---GPEINEELM 256
439 RAMTSIXGQLAGIKELGLDQVSYITGASGSTYALANLIEDPMSOKDLAQPTEL---LK 495
257 KVNSHNPLLLLPQKVRVYESLWKKSSGQPYTFDIFGMLIGETLILHNRMNT-TLSSLI 315
496 TQVTKKRLGLVAPSLQVRROELARARLGYPCFTLWNA-LINEALLHDEPHDKLSQ 554
316 KEKVNTAGCPPLFTCLAHK-PDVSELMAADVVEESPTEIGMAKYTFMAPDLFGSKFTN 374
555 REALSHGQNPPLPYCALNLNKGSILTFEFGEWCEFSPEYEGPKYGAFTPSELFGSEFFM 614
375 GTVVVKYKEENPLHFLMGVGAFAFSLFNVLVIGSSQSGSRGSTPEEL-----ENTTKH 428
615 GQMKRLPESRJCIEFGIMSNLYA-----ANLDLSLWASEPQFQWDM 658

429 IVSNDSDSD---ESHEPKGTENEDAGSDYOSDNQASWIMHIMIALVSDALNFTREG 484
659 VNRQANLDEKEQVPLKIEEPPSTAGRIA--EFFTD-----LLTWP 697
485 RAGKVNEMIGLANTSTYLSPLSPDFATQDSFDDDELDAVAADPDEFERITEPLDYKSK 544
698 LQATHNFLRGLHFHKDYQHP--HFSTWKATTLQGL-----PNO-----LTPSEPH 742
545 HHVVDGLTFNLPYLLILRQGVDDLIISFDSARPSSDPPFKELLAEKAKNKLPE 604
743 LCLLDVGYLINTSCPLDPTRDVDLILSLDYNLGA-----FOQLQLGRFCQEGITF 797
605 PKIDPYFDPREGLEKCYVER-KPNPMKDCPTIIFVLANINFRKYPKGVPRETEERK 663
798 PPIPSPEEQDLPRECHTFSDPICP---GAPAVLHFLPVSDFREYSAPGV-RRTPEEA 852
664 ELADPFIIDPESPESFTFQYPNQAFKRLHLMFNNTANINDIVIKAVESIEYRQ 721
853 AAGEVNL-SSSDSPYHYTKVTSQEDVDLHLTHYCNQNOELLEALRQAVQRRQ 909

RESULT 5
US-08-890-615-2
Sequence 2, Application US/08890615
Patent No. 6121031

GENERAL INFORMATION:
APPLICANT: Song, Chuanzheng

APPLICANT: Kriz, Ron

TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ENZYMES
TITLE OF INVENTION: AND POLYNUCLEOTIDES ENCODING SAME

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive

CITY: Cambridge
STATE: Massachusetts

COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/890,615
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15300
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-498-8224
TELEFAX: 617-876-5851

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 541 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Active-site
LOCATION: 6..242

FEATURE:
NAME/KEY: Active-site
LOCATION: 366..535

US-08-890-615-2

Query Match 12.7%; Score 499.5; DB 3; Length 541;
Best Local Similarity 27.0%; Pred. No. 1.7e-37;

NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSeq for Windows version 3.0
 SEQ ID NO 10
 LENGTH: 552
 TYPE: PRT
 ORGANISM: Hyphozyma sp. CBS 648.91
 US-09-295-186-10

Query Match 5.1%; Score 200.5; DB 3; Length 552;
 Best Local Similarity 21.5%; Pred. No. 6.9e-10;
 Matches 118; Conservative 76; Mismatches 196; Indels 159; Gaps 24;

154 EKTFRQQRKHEIRSMKLLG-----PKNSEGLHSARD-VPVVAIIISGGGFRAMV 203
 114 EADYVSRFRNTQADMAKMKLSDAKLNSLPGASANTSTDRVPRGLFSLSGGLRAML 173
 204 GFGGVKAL-----YESGILDCATYVAGISGSTMSTLYSHPDPEKGPPEINE 253
 174 VGSOTLOGFGRNETANQRCGTGILLAEYIAGISGSMATASL-----TMNNMATYQ 226
 254 ELKKNVSHNLLLTLPQ--KVKRYVESLKM--KSSGQVTFIDIFGMLIGETLIH--- 305
 227 SLADNTIDLESNLTIVPDGKVSFTASTLAAGVGRNREGYQTSITDYFGLSIADKILGSM 286
 306--NRMNTTSLSK--EKVNTAOCPLPFTCLHVKPDVSELMF---ADWVEFSPEYEGM- 356
 287 YGNKFSVEMSDVAKNTSKFTDASMPFIIDNEHP--GELLIRNTIIM-EFNPYEGSM 343
 357-AKGTFTMAADLGSKFFMGT-----VYKKEENPLHLMGWSABSEILNRYLGVS 408
 344 NPVSAPIELPIGLSSLDNCTSVLPDGVCGGYE--TVAWVTGISATLFGLYLELI--- 398
 409 GSGSRGSTESELENTITTKHIVSNDSDSDSESHPKGTENEDAGSDYQSDNQASWIRHM 468
 399--STSSNNIYDALKEL--QAVSNEQND----- 423
 469 IMALVSDSALFNTREGRAGVHNFMLGLNLTSPISPLSDFAFDQSFDDDELDAAYADP 528
 424--VSLVP-----NPFYGYVG-----EGDVQYSD- 444
 529 DEFERITEPDKVSKKHVVDGSL--TFNLTPYPLLRQBGVDLISDFESARSD--SSP 585
 445-----LRNTTLVDGGIDNENVPMLPLVEPARDLVIALIDSSADVTNNMPNAS 491
 586 PFKEILAEKWMKMKLPFKI--DPYVDEREGLEKCYVFKPKPMDMKDPTIIFEVIAN 644
 492 ALVQTSIRAGYPTYQVAFVPMPTNTVVRGLNTRPVF-----YGCNATVYVNTNAD 543
 645 INFRKYKAP 653
 544 TSFNGTKTP 552

RESULT 12
 US-08-609-049A-16
 Sequence 16, Application US/08609049A
 Patent No. 5948664
 GENERAL INFORMATION:
 APPLICANT: Williams, Lewis T.
 APPLICANT: Moiz, Lisa
 APPLICANT: Chen, Yen-Wen
 TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,049A
 FILING DATE: 29-FEB-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Karen B.
 REGISTRATION NUMBER: 29,684
 REFERENCE/DOCKET NUMBER: 2307K-063700US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 140 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-609-049A-16

Query Match 2.8%; Score 112; DB 2; Length 140;
 Best Local Similarity 30.6%; Pred. No. 0.0098;
 Matches 30; Conservative 21; Mismatches 37; Indels 10; Gaps 5;

43 DPYVELFI--STPPDRKRRHFNNDINPYWNETFEF--ILDPN-QENVLETIMDMAN-Y 96
 47 DPYVKHLPLGASKSMKRLKTLNTRNPIWNETLVYHGTTDDMKRKTLLRSVCEDEXF 106
 97 VMDETLGATFTVSSMKVGEKEVPEIFNQVTEVLEM 134
 107 GHNEFIEGTFSLKLLKPNQRKN-----FNICLERVLP 140

RESULT 13
 US-08-095-737-4
 Sequence 4, Application US/08095737
 Patent No. 5487979
 GENERAL INFORMATION:
 APPLICANT: DiFiore, Pier P
 APPLICANT: Fazio, Francesca
 TITLE OF INVENTION: A Substrate for the Epidermal Growth
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knodbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive, Sixteenth Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: United States of America
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/095,737
 FILING DATE: 19930722
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelson, Ned A.
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NH060.001A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 897 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-095-737-4

Query Match 2.7%; Score 108; DB 1; Length 897;
Best local Similarity 20.2%; Pred. No. 0.55;
Matches 100; Conservative 60; Mismatches 203; Indels 132; Gaps 20;

QY 210 KALYESGIL---DCATYVAGLSGSGTWYMT-----LYSHDPPEKGP----- 248
DB 225 KARYDEFLTKDMDGYVSGLEVRETFKTLGPSALLAHWISLQDKGCKLSKQFAL 284
QY 249 --EINEELKKNVSHNPLLLTPQKRYVESLMKKSSG-QPVTFTDIFGMLIGETL-- 303
DB 285 AFHLINOKLIKGI--DPHSLTPEMIPPSDRSSLQKNITSSPV--ADFAIKELDTLNN 340
QY 304 ---IHNRMTTSLSKKVNFAOCPLEFTCLHVKPDVSELM-FADWVEFSPEYIGMAK 358
DB 341 EIVDLQREKNNVBODLKEKEDT-----VKQRTSEVODLQDEVQRESINLQKIQ 388
QY 359 YGTFMAPDLFGSKFPMGTGVKKYEENPLHFLMGWGSASFILNRYLVGSGSGSGSTME 418
DB 389 AOKQOYVELLIGEL---DEQKQALEQLEQLEVRKKCAEAOGLISLKAETISQESQISSYE 444
QY 419 -----ELENITTKHIVSNDSSDSDSHPEKGTENEDAGSDYOS----- 458
DB 445 EELIKAREELSRLOQETAOLESEVSGKQALEPQOHLQSOEISSMOKRLEMKDLETD 504
QY 459 DNQASWIRHIMALV---SDSALFNTREGRAKVHNFMLGLNNTSYLSPLS-----D 509
DB 505 NQOSNMSSSPQSVLVNATGYCISLTSSSETANFNENAEQONNLESPTHOESSVRSPE 564
QY 510 FARQDSFDDDELDAVA-----DPDEFERIEPLDVSKKI--HYVDSGLTFNLPLP 559
DB 565 IASDVYDESEAVTVAGNEKVTFRFDDKHSKEEDPENVSSSLTDAVADTNLDF----- 619
QY 560 LILRPQGVLLISFDSARPSSDPFKELLAEKAKKNNKLPFPKIDYVVDREGLKE 619
DB 620 -----FQSDPEVGSDFPKD-----DPFGKIDPFGGD----- 645
QY 620 CYVEFKPNPDMKDC 634
DB 646 --PFKGSDF--FASDC 657

RESULT 14
US-08-480-145-4
Sequence 4, Application US/08480145
Patent No. 5717067
GENERAL INFORMATION:
APPLICANT: DiFiore, Pier P
APPLICANT: Fazio, Francesca
TITLE OF INVENTION: A Substrate for the Epidermal Growth
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth floor
CITY: Newport Beach
STATE: California
COUNTRY: United States of America
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,145
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/095,737
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH060.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 897 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-145-4

Query Match 2.7%; Score 108; DB 1; Length 897;
Best local Similarity 20.2%; Pred. No. 0.55;
Matches 100; Conservative 60; Mismatches 203; Indels 132; Gaps 20;

QY 210 KALYESGIL---DCATYVAGLSGSGTWYMT-----LYSHDPPEKGP----- 248
DB 225 KARYDEFLTKDMDGYVSGLEVRETFKTLGPSALLAHWISLQDKGCKLSKQFAL 284
QY 249 --EINEELKKNVSHNPLLLTPQKRYVESLMKKSSG-QPVTFTDIFGMLIGETL-- 303
DB 285 AFHLINOKLIKGI--DPHSLTPEMIPPSDRSSLQKNITSSPV--ADFAIKELDTLNN 340
QY 304 ---IHNRMTTSLSKKVNFAOCPLEFTCLHVKPDVSELM-FADWVEFSPEYIGMAK 358
DB 341 EIVDLQREKNNVBODLKEKEDT-----VKQRTSEVODLQDEVQRESINLQKIQ 388
QY 359 YGTFMAPDLFGSKFPMGTGVKKYEENPLHFLMGWGSASFILNRYLVGSGSGSGSTME 418
DB 389 AOKQOYVELLIGEL---DEQKQALEQLEQLEVRKKCAEAOGLISLKAETISQESQISSYE 444
QY 419 -----ELENITTKHIVSNDSSDSDSHPEKGTENEDAGSDYOS----- 458
DB 445 EELIKAREELSRLOQETAOLESEVSGKQALEPQOHLQSOEISSMOKRLEMKDLETD 504
QY 459 DNQASWIRHIMALV---SDSALFNTREGRAKVHNFMLGLNNTSYLSPLS-----D 509
DB 505 NQOSNMSSSPQSVLVNATGYCISLTSSSETANFNENAEQONNLESPTHOESSVRSPE 564
QY 510 FARQDSFDDDELDAVA-----DPDEFERIEPLDVSKKI--HYVDSGLTFNLPLP 559
DB 565 IASDVYDESEAVTVAGNEKVTFRFDDKHSKEEDPENVSSSLTDAVADTNLDF----- 619
QY 560 LILRPQGVLLISFDSARPSSDPFKELLAEKAKKNNKLPFPKIDYVVDREGLKE 619
DB 620 -----FQSDPEVGSDFPKD-----DPFGKIDPFGGD----- 645
QY 620 CYVEFKPNPDMKDC 634
DB 646 --PFKGSDF--FASDC 657

RESULT 15
US-08-477-389-4
Sequence 4, Application US/08477389
Patent No. 5872219
GENERAL INFORMATION:
APPLICANT: DiFiore, Pier P
APPLICANT: Fazio, Francesca
TITLE OF INVENTION: A Substrate for the Epidermal Growth
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth floor

Search completed: July 31, 2001, 16:30:09
Job time: 56 sec

CITY: Newport Beach
STATE: California
COUNTRY: United States of America
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 789
APPLICATION NUMBER: US/08/477,389
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/095,737
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH060,001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 897 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-389-4

Query Match 2.7%; Score 108; DB 2; Length 897;
Best Local Similarity 20.2%; Pred. No. 0.55;
Matches 100; Conservative 60; Mismatches 203; Indels 132; Gaps 20;

OY 210 KALYESGIL---DCATYVAGLSGSTMVST-----LYSHDPPEKGP----- 248
DB 225 KAKYDEIFLTKDMDGVSGLEVRETFKLTGLPSALAHIMSLDPTKCGKLSKQDFAL 284
OY 249 --EEINEELMKVSNHPLLLTPQVKRYVESLMKKSSG-QPYTFDTLFGMLIGETL-- 303
DB 285 AFHLINOKLIKGI--DPRHSLTPEMLPPSDRSSLOKNITGSSPV--ADPSAIKELDTLNN 340
OY 304 ----IHNRNNTLSSLKEKVTACPLPLFTCLHYKPDVSELM-FADWVEFSPEYIGMAK 358
DB 341 EIVDLQREKNNEQDLKEDETF-----VKQRTSEVODLQDEVQRESINLQKIQ 388
OY 359 YGTFMAPDLFGSKFMGTIVVKRYEENPLHFLMGVWSAFSILFNRYLGVSGSOSRGSTME 418
DB 389 AOKQOVQELLGEL---DEOKAQLEBQLQEVRRKCAEEAQLISLKAETTSQESQISSYE 444
OY 419 -----ELENITTKHYISNDSSDDESHPEKGTENEDAGSDYOS----- 458
DB 445 EELLAREELSLRLOQETALQLESVESGKAQLEPLQOHLQESQOELISSMQMRLEMKDLETD 504
OY 459 DNQASWIRHIMIALY---SDSALFMTREGRAGKVHNFMLGLNLTSTYPLSPS-----D 509
DB 505 NNQSNMSSSPQSVLVNGATDYCLSTSSSETANFNEHAGQNNLSEPTHQESSVRSASPE 564
OY 510 FATQDSFDDELDAVA-----DPDEFERYEPLDVYSKRI--HVVDSGLTFNLPPY 559
DB 565 IAPSDVTDESEAVTYAAGNEKVTPRFDDOKHSKEEDPFNVNESSLTDVAVDTLNDF----- 619
OY 560 LILRQRGVDLILISFDSARPSDSSPPREKELLAEKMAKMKLPPPKIDPYVFDREGLKE 619
DB 620 -----FQSDPFVGSDDPFKD-----DPFGKIDPFEGD----- 645
OY 620 CYVFKKNDPMKDC 634
DB 646 --PFKGSDF-PASDC 657

CC phospholipase A2 (PLA2) is the common name for phosphatide-2-
 CC acylhydrolase which catalyses the hydrolysis of the sn-2 acyl ester
 CC bond of phosphoglycerides. The most abundant form of PLA2 is the
 CC secreted form. Cytosolic PLA2 is extremely rare so an expression
 CC system was developed to yield larger amts. of the enzyme, which is
 CC thought to be involved in asthma, ischemia, arthritis, septic shock
 CC and inflammatory diseases of the skin. The cDNA sequence of cPLA2
 CC was enzymatically copied from the mRNA found in nature (see
 CC US92301620.8 for details). The cDNA may be inserted into an
 CC expression vector, pref. contg. a promoter, a selectable marker,
 CC a temp. sensitive repressor and other regulatory elements necessary
 CC for transcription and translation in E. coli. The vector may be
 CC used to transform E. coli, which may be cultured to obtain large amts.
 CC of cPLA2. The gene, and the enzyme it encodes may be used to
 CC screen cpds. to identify inhibitors of cPLA2.

XX
 XX
 SO Sequence 749 AA:

Query Match 100.0%; Score 3942; DB 13; Length 749;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFTDPYQHIIYEHQYSHKFTYVVLRAVTYKAGFDMIDTPDYVELFTSTPDSRRKT 60
 DB 1 msftidpyqhlivehqyshkftvvlratkvtkagfdmldtpdyvelftstpdskrt 60
 QY RHNNNDINVMNTEFEELIDPNQENLEITLMDANVMDETGTAFPTYSMKVGEKKEY 120
 DB 61 rhnnndinvmntefelldpnqenvleltmdaanyvmetlgtafptysmkvgekkev 120
 QY 121 PFIENOVTEVLEMSLEVCSPDLRFSMALCDQEKTFROORKEHIESMKKLGPKNSEK 180
 DB 121 pfienovtevmlemslevcspdlrfsmalcdqektfrroorkehiesmkkllgpknses 180
 QY 121 pfiingvtemvlemalesvcspdlrfsmalcdqektfrgrkhesmkkllgpknses 180
 DB 181 lmsarvpyvvaillgsggrawgescvkmakalyesgilldcattyaglsstgwtmstlysh 240
 DB 181 lmsarvpyvvaillgsggrawgescvkmakalyesgilldcattyaglsstgwtmstlysh 240
 QY 241 PDPEKGPPEINELMKNSHNPILLTLTPQKRYVESLWKKSSGSCOPTFTDIPMLIG 300
 DB 241 pdpekgppeinelmknsnhnpilltltpqkryveslwksssgscoptftdipmlig 300
 QY 301 ETLIHRMNTTSLSEKYNVTAQCLPFTCLHVKKPDVSELMFADWERSPYEIGMAKYG 360
 DB 301 etlihrmnttsslsekynvtaqcplpftclhvkcpdvselmfadwvetspyelgmkayg 360
 QY 361 TRFAPDLFGSKFFMGTVVKKYEBNPLHFLMGWGSFSLFNRYLGVSGSQSGSTWEEB 420
 DB 361 trfapdlfgskffmgtvvkkyyebnplhflmgwgsfslfnrylgvsgsqsgstwmese 420
 QY 421 LENITTKHIVNSDSDSDSHSEPKGTENDAGSDYQSDNQASWIRHIMLVALVSDALFN 480
 DB 421 lenittkhivnsdssdsdshsepkgtendagsdyqsdnqaswlrmalvalvdsalln 480
 QY 481 TREGRAGKYVHNFMLGLNLTSTYPLSLSDFATQDSFDDDELDAVAADPDEFERIYELDV 540
 DB 481 tregragkvhnmfmlglnltsyplslsdfatqdsfdddeladaavadpdeferyelpldv 540
 QY 541 KSKKIVVNSGLTFNLPYLILRPQGVDLISFDSARPSSDSPPFKELLAEKAKANN 600
 DB 541 kskkivvnsgltnlpylilrpqgvdlisfdsarpsdsppfkellaeakakann 600
 QY 601 KLPFPKIDYVFDREGLKECYVFKPKNPMEXDCPTIIHFVLANINFRKYKAPGVRETE 660
 DB 601 klpfpidyvfvdreglkecyvfkpknpmekdcpitihfvlaninfrkykagvprete 660
 QY 661 EEKEIADFDIDDPESPSTFTFNQYDQNAQFKRLHDLMHENTLNIDVIEKAWESIERYR 720
 DB 661 eekeiadfdiddpespfstftfnqypnagfkrldlmhfnltnidviekawesleyrr 720
 QY 721 QNPSCSVLSNVEARRFNRKFLSKPKA 749
 DB 721 qnpscsvlsnvearrfnrkeflskpkA 749

DB 721 qnpscsvlsnvearrfnrkeflskpkA 749

RESULT 2
 ID AAR63757 standard; Protein; 749 AA.

AC AAR63757;

DT 09-JUN-1995 (first entry)

XX Human phospholipase A2 (PLA2).

XX Intracellular phospholipase A2; PLA2; anti-inflammatory chemicals;
 KW prostaglandin leukotriene regulation; platelet activating factor.
 XX
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers

FX Peptide 414..427

FT /note= "tryptic fragment used to design
 the oligonucleotides"

FT Peptide 534..0

FT /note= "tryptic fragment"

FT Peptide 599..601

FT /note= "tryptic fragment"

FT Peptide 607..613

FT /note= "tryptic fragment"

FT Peptide 649..656

FT /note= "tryptic fragment used to design
 the oligonucleotides"

FT Peptide 710..718

FT /note= "tryptic fragment"

PN US5354677-A.

XX 11-OCT-1994.

PD 28-FEB-1990;

PF 90US-0486628.

PR 28-FEB-1990;

PR 90US-0486628.

PR 13-JAN-1993;

PR 93US-0002447.

PA (GENY) GENETICS INST INC.

PA Clark J, Knopf JL;

PI WPI, 1994-324553/40.

DR N-PSDB; AAO74416.

XX Claim 1; Columns 5-10; 13pp; English.

PT Intracellular phospholipase A2 - used in methods for detecting
 the anti-inflammatory potential of various chemical agents

PS The cDNA sequence AAO74416 encodes AAR63757, biologically active

CC human phospholipase A2 (PLA2). This enzyme can be used to

CC determine the anti-inflammatory potential of various chemical

CC agents. PLA2 also displays enzymatic activity in a mixed micelle

CC assay, this activity indicates PLA2's involvement in the regulation

CC of the prostaglandin and leukotriene pathways, and the biosynthesis

CC of platelet activating factor.

XX
 XX
 SO Sequence 749 AA:

Query Match 100.0%; Score 3942; DB 15; Length 749;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFTDPYQHIIYEHQYSHKFTYVVLRAVTYKAGFDMIDTPDYVELFTSTPDSRRKT 60
 DB 1 msftidpyqhlivehqyshkftvvlratkvtkagfdmldtpdyvelftstpdskrt 60

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QY 61 RHEFNNDINPWNTEFEIILDPNENVEITLMDANYMDETLGATFTVSSMKYGEKKEV 120
DB 61 rhfnndinpwnetfeilidpnenveitlmdanymdetlgtatftvssmkvgekkev 120
QY 121 PFTFNQTEVLEKSLVSCGCPDLRFESMALCDQKTRQQRKEHRSRMRKLLGPKNSEG 180
DB 121 pftfnqtevmlekslvscgcpdlrfesmalcdqktrqrkehrrsmrkllgpknsseg 180
QY 181 LHSARDVPVVAIIIGSGGFFAMVGFSGVMKALYESGILDCATYVAGISGSTMWSTLYSH 240
DB 181 lhsardvpvvaillgsggffamvfgsgvmkalysesgildcatyvagisgstwmstlysh 240
QY 241 PDEPEKGEPEINEELMKVSNHPILLTPQVKRYVESLWKKSSGQPVFTDIFGMLIG 300
DB 241 pdepekgepeineelmkvsnhpllltpqvkryveslwkkssgqpvftdiftgmlig 300
QY 301 ETLIHNRMNTTSLKRRKVTACQPLFLFCLHVKRPVSELMFADWVEFSPYEIGMAKYG 360
DB 301 etlihnrmnttsslkrrkvtaqcplflfclhvkprvselmfadwvefspyeigmakyg 360
QY 361 TFMAPDLFGSKFPMGTWVKKYEENPLHFLMGVMSAFSILFNRYLGVSGSOSRSTWEE 420
DB 361 tfmapdlfgskfpmgtwvkkyeenplhflmgvmsafsilfnrylvgsgsostwee 420
QY 421 LENITTKHIVSNDSDSDSHPEKGTENEDAGSDYOSDNQASWIRHMALVSDSALFN 480
DB 421 lenittkhivsndsdsdshpekgtenedagsdyosdnqaswihrmalvdsalfn 480
QY 481 TRGRACKVHNFMGLNLTSTPLSDPATQDSFDDDELDAVADPDERIYERLDV 540
DB 481 trgrackvhnfmglntstplsdpatqdsfdddeldaavadpderiyepldv 540
QY 541 KSKKIHVVDGILFENLIPYLIRPQRGVDLISDFARSDDSPPKELLAEKAKMN 600
DB 541 kskkihvdsgilfenlpylirpqrgvdlisdfarsddspkellaeakamn 600
QY 601 KLPEPKIDPVFDRREGLEKCYVEFKPNPDMEKDCPTIIHFVLNINIRKRYKAPGPRETE 660
DB 601 klpepkidpvfdrreglekecyvefkpnpdmekdcpitihfvlninirkykagprete 660
QY 661 EEEELADFDIFDPDESPESFTFNQOAFKRLHDLHFNTLNNIDVYKEAMVESIEYR 720
DB 661 eeeeladfdifdpdespfstfnqoafkrlhdlhfntlnnidvykeamvesieyrr 720
QY 721 QNPSRCSVSLSNYEARFEKPELSKPKA 749
DB 721 qnpsrcsvslsnyearfekeplskpka 749

```

RESULT 3

AAR97751 standard; Protein: 749 AA.

AAR97751:

28-AUG-1996 (first entry)

Human phospholipase A2.

Phospholipase A2; PLA2; antiinflammatory.

Homo sapiens.

US5527698-A.

18-JUN-1996.

28-FEB-1990; 90US-0486628.

28-FEB-1990; 90US-0486628.

13-JAN-1993; 93US-0002447.

22-JUN-1994; 94US-00263861.

```

XX (GEMV ) GENETICS INST INC.
PA Clark J, Knopf JL;
PI WPI; 1996-299858/30.
DR N-PSDB; AAR29822.
PT Purified mammalian cytosolic phospholipase A2 - useful to identify
PT anti-inflammatory cpds.
PS Claim 1; Column 5/6-9/10; 13pp; English.
XX A cytosolic phospholipase A2 (PLA2) (AAR29822) was identified as
CC the product of a cDNA clone (AAR29822) isolated from a cDNA
CC library derived from human U937 cells. The PLA2 can be
CC expressed in transformed or transfected bacterial, yeast, mammalian
CC or insect host cells. The specific activity of the PLA2 is approx.
CC 20 umol/min.mg in the mixed micelle assay. The enzyme is useful
CC for identifying antiinflammatory cpds. by determining if the cpd.
CC inhibits PLA2 in cleaving a phospholipid to release fatty acids
CC in a mixed micelle assay, a system using natural enzymes or in
CC whole cells overexpressing the enzyme.
SQ Sequence 749 AA:
Query Match 100.0%; Score 3942; DB 17; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFIDPYOHAIIVEHOYSHKFTVVVLRAATKYTKGAFGMDLTPDPYVELISTTPDSHKRT 60
DB 1 msfidpyqhliivehoyshkftvvlratkytkgafgmdltpdpvelisttpdskrt 60
QY 61 RHEFNNDINPWNTEFEIILDPNENVEITLMDANYMDETLGATFTVSSMKYGEKKEV 120
DB 61 rhfnndinpwnetfeilidpnenveitlmdanymdetlgtatftvssmkvgekkev 120
QY 121 PFTFNQTEVLEKSLVSCGCPDLRFESMALCDQKTRQQRKEHRSRMRKLLGPKNSEG 180
DB 121 pftfnqtevmlekslvscgcpdlrfesmalcdqktrqrkehrrsmrkllgpknsseg 180
QY 181 LHSARDVPVVAIIIGSGGFFAMVGFSGVMKALYESGILDCATYVAGISGSTMWSTLYSH 240
DB 181 lhsardvpvvaillgsggffamvfgsgvmkalysesgildcatyvagisgstwmstlysh 240
QY 241 PDEPEKGEPEINEELMKVSNHPILLTPQVKRYVESLWKKSSGQPVFTDIFGMLIG 300
DB 241 pdepekgepeineelmkvsnhpllltpqvkryveslwkkssgqpvftdiftgmlig 300
QY 301 ETLIHNRMNTTSLKRRKVTACQPLFLFCLHVKRPVSELMFADWVEFSPYEIGMAKYG 360
DB 301 etlihnrmnttsslkrrkvtaqcplflfclhvkprvselmfadwvefspyeigmakyg 360
QY 361 TFMAPDLFGSKFPMGTWVKKYEENPLHFLMGVMSAFSILFNRYLGVSGSOSRSTWEE 420
DB 361 tfmapdlfgskfpmgtwvkkyeenplhflmgvmsafsilfnrylvgsgsostwee 420
QY 421 LENITTKHIVSNDSDSDSHPEKGTENEDAGSDYOSDNQASWIRHMALVSDSALFN 480
DB 421 lenittkhivsndsdsdshpekgtenedagsdyosdnqaswihrmalvdsalfn 480
QY 481 TRGRACKVHNFMGLNLTSTPLSDPATQDSFDDDELDAVADPDERIYERLDV 540
DB 481 trgrackvhnfmglntstplsdpatqdsfdddeldaavadpderiyepldv 540
QY 541 KSKKIHVVDGILFENLIPYLIRPQRGVDLISDFARSDDSPPKELLAEKAKMN 600
DB 541 kskkihvdsgilfenlpylirpqrgvdlisdfarsddspkellaeakamn 600
QY 601 KLPEPKIDPVFDRREGLEKCYVEFKPNPDMEKDCPTIIHFVLNINIRKRYKAPGPRETE 660
DB 601 klpepkidpvfdrreglekecyvefkpnpdmekdcpitihfvlninirkykagprete 660

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DB 601 klpfkipdyvidreglkecyvfkpknpmekdcpllnfvlanlnfkykapyvprete 660
OY 661 EEKEIADFDIDDPESPFSFNFQYPNQAFKRLHDLHFNLTNNIDVYKEAWVESTLEYR 720
DB 661 eekeiadfdidfpespfscfnfyqpnqafkrlhnlmhnlnldvlykeawvestleyr 720
OY 721 QNPSRCSVSLSNVEARFRFNKEFLSKPKA 749
DB 721 qnpsrcsvslsnvearrrfnkeflskpka 749

RESULT 4
AAW11607
ID AAW11607 standard; Protein; 749 AA.
AC AAW11607;
DT 07-OCT-1997 (first entry)
DE Human phospholipase A2 enzyme.
DE Human; PLA2; anti inflammatory; drug development; antibody.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 14..427
FT /label= Tryptic_fragment 534..540
FT /label= Tryptic_fragment 599..601
FT Region /label= Tryptic_fragment 607..613
FT Region /label= Tryptic_fragment 649..656
FT Region /label= Tryptic_fragment 710..718
FT Region /label= tryptic_fragment

US5593878-A.
PN 14-JAN-1997.
PF 28-FEB-1990; 90US-0486628.
PR 28-FEB-1990; 90US-0486628.
PR 13-JAN-1993; 93US-0002447.
PR 22-JUN-1994; 94US-0263590.
PA (GENW ) GENETICS INST INC.
PI Clark J, Knopf JL;
PI MPI: 1997-099471/09.
PI DR N-PSDB; AAT61187.
PT New murine phospholipase A2 enzymes - useful for developing
PT anti-inflammatory drugs
PS Example 4; Column 5-8; 22pp; English.
XX The present sequence represents human phospholipase A2 enzyme (PLA2).
XX The human sequence shares significant similarity to protein kinase
XX C-gamma, indicating a common function. The function is likely to include
XX the regulation of the enzyme by calcium and the calcium dependent
XX binding to membranes. The tryptic fragments, indicated in the features
XX table, were subjected to automated gas phase microsequencing as part of
XX the protein sequencing analysis of the human PLA2. The PLA2 enzyme is
XX used for detecting the anti-inflammatory potential of various chemical
XX agents, and for developing new drugs. Antibodies to PLA2 may be used
XX diagnostically, in research and for treating inflammatory conditions.
SQ Sequence 749 AA.
```

```
Query Match 100.0%; Score 3942; DB 18; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSFIDPYQHIIIEHOYSHKFTVVLNATKVTGAFGDMLDTPDYVELFISTTPDSRKRT 60
DB 1 msfidpyqhliivehgyshkftvvlratkvctkgafgdmldtpdyvelfisttpdsrkt 60
OY 61 RHFNNDINFWMETFEFILDPNQENVLETITMDANTVMDETLGATFTYSSKAGVEKKEV 120
DB 61 rhfnndinfwmetfeildpnqenvletitmdantvmdetlgtatfvysskagvekkev 120
OY 121 PFENOVTEWVLEMSLEVCSCPDLRFSNALCDEKTEFROCKEHTRESKKTLLGKRNSEG 180
DB 121 pfenovtewvlemslevcscpdlrfsnalcdtektefrckehreskktllgkrsneg 180
OY 181 LHSARDVPVAILGSGGFRAMVGFSGVKKALYESGILDCAATYVAGLSGTYWNSTLYSH 240
DB 181 lhsardvpvailgsggframvgfsgvkkalysesgildcaatyvaglsgstywnstlysh 240
OY 241 PDPPEKGPEEINDELMKNSHNPDLILTPQKRYRYVESLMKKSSGQPTFTDIDGMLIG 300
DB 241 pdppekgpeeindeilmknshnpdliltpqkryryveslmkksqgptftdldgmlig 300
OY 301 ETLIHRMNTTSLSEKKNYTAQCPLEPTCLHVPDVSLEMFADWVERSPYEIGMAKYG 360
DB 301 etlihrmnttsslsekknnytacpleptclhvpdvslemfadwverspyeigmakyg 360
OY 361 TFWAPDLFGSKFFPMGTIVVKKYEBNPLHFLMGVGSASFILFNRYLGVSGSGSGSTMEBE 420
DB 361 tfwapdlfgskffpmgtivvkkyebnplhflmgvggsasfiflnryylgvsgsgstmebe 420
OY 421 LKNITTKHIVSDSSDSDESHPEKGTENEDAGSDYQSDNQASWIRMTALVVSALFN 480
DB 421 lknittkhivsdssdsdeshepkgtenedagsdyqsdnqaswlrmtalvvsalfn 480
OY 481 TREGRAGKVNFMGLNLNTSYPLSPDFAQTDSFDDDELAAVADPDEFRIYEPILDV 540
DB 481 tregragkvnmglnlntsyplspdfatqdsfdddelaaavadpdeferiyepildv 540
OY 541 KSKKIHVDSGLTFNLPYLLIRPQGVLDLISFDSNAPSSSPPEKLLLAEKWAKKN 600
DB 541 kskkihvdsgltnlpylirpqgvldlisdnsapssppeklllaekwakkn 600
OY 601 KLPFPIIDPYVDREGLKCYVFKPNPMEKDCPTIIHFVLANINFRKAKAGVPRETE 660
DB 601 klpfpidpyvidreglkecyvfkpnpmekdcpilnfvlanlnfrykagvprete 660
OY 661 EEKEIADFDIDDPESPFSFNFQYPNQAFKRLHDLHFNLTNNIDVYKEAWVESTLEYR 720
DB 661 eekeiadfdidfpespfscfnfyqpnqafkrlhnlmhnlnldvlykeawvestleyr 720
OY 721 QNPSRCSVSLSNVEARFRFNKEFLSKPKA 749
DB 721 qnpsrcsvslsnvearrrfnkeflskpka 749

RESULT 5
AAW14650
ID AAW14650 standard; Protein; 749 AA.
AC AAW14650;
DT 28-JUL-1997 (first entry)
DE Human phospholipase A2 (PLA2).
DE Human phospholipase A2 (PLA2).
DE Phospholipase A2; PLA2; inhibitor; inflammation;
DE antiinflammatory.
OS Homo sapiens.
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XX Key Location/Qualifiers
FH Peptide 414..427
FT /Label- tryptic_peptide-1
FT Peptide 534..540
FT /Label- tryptic_peptide-2
FT Peptide 599..601
FT /Label- tryptic_peptide-3
FT Peptide 607..613
FT /Label- tryptic_peptide-4
FT Peptide 649..656
FT /Label- tryptic_peptide-5
FT Peptide 710..718
FT /Label- tryptic_peptide-6
XX
XX US562832-A.
XX PD 22-APR-1997.
XX PF 28-FEB-1990; 90US-0486628.
XX PR 28-FEB-1990; 90US-0486628.
XX PA (GEMT ) GENETICS INST INC.
XX PI Clark J, Knopf JL;
XX DR MPI: 1997-244389/22.
XX DR N-PSDB; AAT61758.
XX PT Screening assay for phospholipase A2 inhibitors - using
XX PT phospholipase A2 encoded by defined DNA sequence
XX PS Claim 1; Columns 5-8; 12pp; English.
XX
CC A human phospholipase A2 (PLA2) (AAW14650) has a specific activity
CC of 20 umol/min/mg in mixed micelle assay. It can be produced in
CC mammalian, insect or bacterial hosts utilizing a cDNA clone
CC (AAT61758) obtd. from a human monocyte U937 cDNA library using probes
CC based on human PLA2 tryptic peptides (see also AAW14652-56). Human
CC and murine PLA2 (see also AAW14651) can be used in screening assays
CC for cpds. capable of inhibiting the action of PLA2 in cleaving a
CC phospholipid to release fatty acids. Such inhibitory activity is
CC indicative of use as an antiinflammatory.
CC
XX Sequence 749 AA:
SQ

```

```

Query Match 100.0%; Score 3942; DB 18; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MSFIDYOHITVHOYSHKRTVVVLATKTKGAFGMDTPPYVELFISTPDSKRT 60
DB 1 msfIdyqhIvHqYshKrtVvVLATkTKgAfGmDtpPyVeLfIstPdSkRt 60
QY 61 RHFNDINPYWNETFEFIIIDPNOENVLEITLMDANYMDETLTAFTVSMKGEKEV 120
DB 61 rhfndInpywnetfeIIIdpNoEnvLeITlMDAnYmDeTLtAftVsmKgeKeV 120
QY 121 PFIPOVTEKMLESLVSCSPDLRFSMALCDDEKTFRQQRKHIRESMKLLGPKNSEG 180
DB 121 pfIpoVteKmlEslVscSPdlRfSmAlCdDeKtFRqQRKhIReSmKllGpKnsEG 180
QY 181 LHARQVPAVAILIGSGGFAPAMGFGVMKALYESGTLDCATVAGISGSTWSTLYSH 240
DB 181 lHaRQvPAvAILIGSGGFaPAMGFGVMKaLYeSGtlDcATvAGISGStwStLySh 240
QY 241 PDEPEKGPPEINELMKMNSHNPILLTPQKRVRYESLKKKSSGQPVFTTIFGMLIG 300
DB 241 pdEpeKGPpEINeLMkMNShNPILLtpQkRVryESlKKKSSGQpVFTtIFgMLIG 300
QY 301 ETLIHNRMNTTSSLKEKVTFAOCPLEFTICLHVKPDVSELMFADWVERSPYEIGMAKYG 360

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DB 301 eTLIHnRMntTSSlKeKvTfAOcPlEftIClHvKpDvSElMfADwVERSPyEIGmAKyG 360
QY 361 TFWAPDLFGSKPFMGTVYKKYEENPLHFLMGVWGSFSLFNFNLGVSGSQSGSTMEEE 420
DB 361 tFwApDLfGskPfMGtVYkKyeENpLhFlMGvWGSfSLfNfNLgVSGsGSSTmEEe 420
QY 421 LENITTKHIVSDSDSDSHKPKCTENEDAGSDYQSDNQASWIRMTALVSDSALFN 480
DB 421 lenITtkHivsdSDsdshKpKctENeDAGsDYqSDnQASwIRmTAlVsdSaLfN 480
QY 481 TREGRAGKYNHFMGLNLTSTYPLSLSDFAQDSTDDDELAAVADPPEFEKITYPLV 540
DB 481 tReGrAgKynHfMGLnLTstYpLsLsdFAqDSTddDELAAvADpPeFEkItYpLv 540
QY 541 KSKKHVDSGLTFENLPYPLILRPGVYDILISFDSARPSSDPPEKELLAEKKAKMN 600
DB 541 kSkKhVdsGLtFnlPyPlILrPgVdILIsfDsArPssDPpEkElLaEkKaKmn 600
QY 601 KLPFPKIDPYVEDREGIJEQYVFKPRNPDMKDCPTLIHFLVANIINFRKYPKAPVRETE 660
DB 601 kLpFpKiDpyVeDReGijEqYvFkPrNPdMKdCpTLiHfLVAniInFRkYpKaPvReTe 660
QY 661 EEKEIADFDIDPESPFSTFNFQYPRNOAFKRLHDMHFWTLNNIDVYKAMVESTIEYR 720
DB 661 eeKeIAdfdIdDpEsPfStFnfQyPrNoAFkRLhDMHfWtLnnIdVYkAmVeStIEyR 720
QY 721 QNPSCSVLSNVEARFPEKFLSKPKA 749
DB 721 qNpScSVlSnVeArFfPeKfLSKpKa 749

```

RESULT 6

AA59631 standard; Protein; 749 AA.

AA59631;

23-MAR-2000 (first entry)

Human phospholipase A2 group IV protein sequence.

Phospholipase A2 group IV; PLA2; antisense compound; inhibit; tumour; infection; inflammation.

Homo sapiens.

US6008344-A.

28-DEC-1999.

23-FEB-1999; 99US-0255893.

23-FEB-1999; 99US-0255893.

(ISIS-) ISIS PHARM INC.

Bennett CF, Cowsett LM;

WPI: 2000-086226/07.

N-PSDB; AAZ56051.

Antisense oligonucleotides inhibit expression of human phospholipase A2 group IV, useful for diagnosis, treatment and prevention of tumours, infection and inflammation -

Disclosure; Column 41-46; 32pp; English.

This is the human phospholipase A2 (PLA2) group IV protein sequence. Phospholipase A2 group IV is activated in response to extracellular stimuli, including growth factors, cytokines, and interferons. The invention relates to an antisense compound which is targeted to the coding region or 5' or 3' untranslated region of PLA2 group IV nucleotide

CC sequence. The antisense compound inhibits the expression of PLA2 group
CC IV. The PLA2 group IV antisense compounds are used to inhibit the
CC expression of cytosolic PLA2 in cells and tissues in vitro. The antisense
CC molecules can also be used to treat or prevent PLA2-associated diseases,
CC particularly infection, inflammation and tumours. The antisense compound
CC can also be used for research or diagnosis, e.g. to study gene function
CC or in hybridization assays.

XX
XX
SQ Sequence 749 AA:

Query Match 100.0%; Score 3942; DB 21; Length 749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 749; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSFIDPYQHIIYEHQSHKFTYVVLKATKVTGAFGMDLDPDPVVELFISTPDSRRKT 60
DB 1 msfidpyqhiiyehqshkftvvlratkvkgaigmdldpdpvvelfstpsdrkt 60
OY 61 RHFNDINPVNMEFEFILDPNQENVLEITLMDANYVDELTGATATVSSMKVGEKKEV 120
DB 61 rhfndinpvnmefefildpnqenvleltlmdanyvdeltgatattvssmkvgekkev 120
OY 121 PRFNOVTVMLEMSLEVSCPDLPFSMALCDQEKTFROQRKEHRESKKLLGEPNSEG 180
DB 121 prfnovtvmlemslevscpdlprfsmalcdqektfrqqrkehresmkllgpnseg 180
OY 181 LHSARDVPVVALISGGGFRAMVFGSVKAKALYESGILDCATYVAGLSGSTMVMSLYSH 240
DB 181 lhsardvpvvalisgggframvfgsvkalkayesgildcatyvgslsgstvmmslysh 240
OY 241 PDPEKGPPEINEELMKVNSHNPILLTPQVKRYVESLMKKSSGQPTFTDIFGMLIG 300
DB 241 pdpekgppeineelmkvnshnpilltpqvkryveslmkkssgqptftdifgmlig 300
OY 301 ETLIHNRMNTTSLSEKYNVTAQCPLFTCLHVRKPDVSELMFADWVESPYEIGMANYG 360
DB 301 etlinhnmnttsslsekynvtaqcplftclhvrkpdvselmfadwvespyeigmakyg 360
OY 361 TFMAPDLFGSKFFMGTVVKKYEENPLHFLMGVGSASFILFNRVLGVSQSRSRGTMEEE 420
DB 361 tfmapdlfgskffmgtvvkkyeenplhflmgvgsasfllfnrvgvsqrsrgtmeee 420
OY 421 LENTTKTHIVNSDSDSDSHSEPKGTENEDAGSDYQSDNQASWIRMTALVSDSALFN 480
DB 421 lenttkthivnsdssdsdshsepkgtenedagsdyqsdngswlrmalvsdsalfn 480
OY 481 TREGRAGKHNHPLGLNLTSTPLSPFATQDSFDDELDAAVADPDEFETIYPLAY 540
DB 481 tregragkhnhplglntstplspfatqdsfddeidaavdpdefetiyleplay 540
OY 541 KSKKIHVNSGLTFNLPYLILRPQGVDLISFDSAPRSDSSPPFEKLLAEKAKANN 600
DB 541 kskkihvnsgltnfnylilrpqgvdlisfdsaprsdssppfekllaekakann 600
OY 601 KLPFPRIDYVDFREGLEKCYVFKPKNPDMKDCPTIIHFVLANINFRKRYKAPGVRETE 660
DB 601 klpfpridyvdfreglekcyvfkpknpmekdcptiifhfvlaninfrkrykapgvrete 660
OY 661 EKEKIDPFIQDPDESPSTFNQYQNAFKRLHDMHNTLNINIDVTEAMVESLEYKR 720
DB 661 ekekidpfiqdpdespstfnqyqnafrklhdmhntlninidvteamvesleykr 720
OY 721 ONPSRCSVLSNVEARFPNKEPLSKPKA 749
DB 721 onpsrcsvlsnvearfpnkeplskpka 749

RESULT 7
AARS4090
ID AARS4090 standard; Protein: 749 AA.
XX
AC AARS4090;

XX
DT 01-FEB-1995 (first entry)
XX
XX PLA2 phospholipase.
DE
XX Phospholipase: inflammatory response; prostaglandin; leukotriene;
KW testing; detection; arachidonic acid; phospholipids; PLA2.
XX
XX Homo sapiens.
OS
XX US5322776-A.
PN
XX 21-JUN-1994.
PD
XX
XX 28-FEB-1990; 90US-0486628.
PE
XX 28-FEB-1990; 90US-0486628.
PR 28-FEB-1990; 90US-0486628.
PR 13-JAN-1993; 93US-0004156.
XX
XX (GENY) GENETICS INST INC.
PA
XX Clark J, Knopf JL;
PI
XX WPT: 1994-199533/24.
DR N-PSDB; AA064162.
DR
XX
XX

PT DNA sequences encoding human and murine phospholipase A2 enzyme -
PT useful for detecting antiinflammatory potential of chemical
PT agents.
PS
XX Claim 1: Columns 5-10; 13pp: English.

CC Prostaglandins and leukotrienes are important mediators of
CC inflammation. They are unstable and are not stored in cells but are
CC synthesised from arachidonic acid in response to stimuli.
CC Arachidonic acid itself is not free in cells but is released from
CC the sn-2 position of membrane phospholipids by phospholipase A2
CC (PLA2). Purified PLA2 can be used in methods for detecting the
CC anti-inflammatory potential of various chemical agents.

XX
XX
SQ Sequence 749 AA:

Query Match 99.8%; Score 3935; DB 15; Length 749;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 748; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSFIDPYQHIIYEHQSHKFTYVVLKATKVTGAFGMDLDPDPVVELFISTPDSRRKT 60
DB 1 msfidpyqhiiyehqshkftvvlratkvkgaigmdldpdpvvelfstpsdrkt 60
OY 61 RHFNDINPVNMEFEFILDPNQENVLEITLMDANYVDELTGATATVSSMKVGEKKEV 120
DB 61 rhfndinpvnmefefildpnqenvleltlmdanyvdeltgatattvssmkvgekkev 120
OY 121 PRFNOVTVMLEMSLEVSCPDLPFSMALCDQEKTFROQRKEHRESKKLLGEPNSEG 180
DB 121 prfnovtvmlemslevscpdlprfsmalcdqektfrqqrkehresmkllgpnseg 180
OY 181 LHSARDVPVVALISGGGFRAMVFGSVKAKALYESGILDCATYVAGLSGSTMVMSLYSH 240
DB 181 lhsardvpvvalisgggframvfgsvkalkayesgildcatyvgslsgstvmmslysh 240
OY 241 PDPEKGPPEINEELMKVNSHNPILLTPQVKRYVESLMKKSSGQPTFTDIFGMLIG 300
DB 241 pdpekgppeineelmkvnshnpilltpqvkryveslmkkssgqptftdifgmlig 300
OY 301 ETLIHNRMNTTSLSEKYNVTAQCPLFTCLHVRKPDVSELMFADWVESPYEIGMANYG 360
DB 301 etlinhnmnttsslsekynvtaqcplftclhvrkpdvselmfadwvespyeigmakyg 360
OY 361 TFMAPDLFGSKFFMGTVVKKYEENPLHFLMGVGSASFILFNRVLGVSQSRSRGTMEEE 420
DB 361 tfmapdlfgskffmgtvvkkyeenplhflmgvgsasfllfnrvgvsqrsrgtmeee 420

D b	361	tftmpdplfgskffmgtyvkvkyeenplhflngwgsatsllfnrlyvsgsgsrstgmnee	420
Q y	421	LENTTKHIVSNDSSDSDSDSHPEKGTENEDAGSDYQSDQASWIRHMALVSDSALFN	480
D b	421	lenlttkhivandsdsdssdeehpekytensedagsdygsdnqaswlrhmalvysdaalfn	480
Q y	481	TREGRACKVNHFMELGLMINTSYPLSPISDRATQDSFPDDELDAVADPDEFERYEPLDY	540
D b	481	tregraqkvnhfmimglhnintsyplspisdfatqgsfddegldaavaodpdeferlyepldv	540
Q y	541	KSXKIHVYDLSGFENLPLPCLIRPQRBVDLIISDFGARPSSDSSPPKELLAEKAKMN	600
D b	541	ksxkihvydsglfclnlpplllrpgqvdlisdfisarspsdpsptkelllaekwakmn	600
Q y	601	KLPPKIDPYPFDRREGLEKECYVFKPKNPDMKDCPTILHVLNINERKKAAGVPETE	660
D b	601	klppkldpypfdtreglkecyvfkrpkndmekdcpthlvlaninerkkaagvprete	660
Q y	661	EKEKEIADFJFDDPESPSTPNFOYPNQAFKRLDLMHFTLNNIDYIKEAWESIETRR	720
D b	661	eeketadfdtfdpessptstfnfygnqafkrlhldmhftlnnidvikeawesieytr	720
Q y	721	ONPSRCVSVLSNVARREFNKEFLSKRKA	749
D b	721	onpsrcsvslsnvarrefnkeflskpka	749

RESULT	8
AAB21142	
ID	AAB21142 standard; protein; 611 AA

19-JAN-2001 (first entry)

Human cytosolic phospholipase A2 cPLA2 alpha.

Human; cytosolic phospholipase A2 alpha; cPLA2 alpha; asthma, arthritis; inflammatory disease; crystal structure.

Homo sapiens.

WO200047763-A1.

17-AUG-2000.

14-FEB-2000; 2000WO-US03745.

15-FEB-1999: 99US-0250083

(GEMY) GENETICS INST INC

Nassen A. Somers WS. Stahl MT. Soehra JS.

WPT: 2000-558219/51

New crystalline cytosolic phospholipase A2 (cPLA2) for identifying a species which is an agonist or antagonist of cPLA2 activity or binding that can be used to prevent or treat inflammation or inflammatory-related conditions -

Disclosure; Fig 4; 71pp; English.

The present sequence is the human cytosolic phospholipase A2 (cPLA2) alpha protein. The invention concerns the elucidation of the crystal structure of the protein and its use in drug design. The protein can be used to identify treatments for inflammation-related conditions such as Rheumatoid arthritis, psoriasis, asthma, Inflammatory bowel disease, and diseases such as osteoporosis, colitis, myelogenous leukaemia, diabetes, and atherosclerosis.

Sequence 611 AA;

Query Match	81.8%;	Score 3224;	DB 21;	Length 611;
Best Local Similarity	100.0%;	Pred. No. 1.2e-293;		
Matches 611;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	139	CSCPLRFSMALCPOEKFRROREHIRESKKILGKNSGJSHADVPVAILISGGG	198
Dd	1	csccpllrfsmalcpcqekfrtqrkxehlrsmkklipgknsesjlshadvpvalisggg	60
QY	199	FRAMVFGSVKALYESGILDCATVYVGLSGSTWMSYTLXSHDPPEKGEETINEELMKN	258
Dd	61	framvfgsvmkalyesgildcatyvvglsgstwmsytlxshdpfpkgeetineelmkn	120
QY	259	VSHNPLLLLTQOKKRYYESLMAKKSSGOPYTFPDIRGMLIGETLHNRKNTLLSLKEK	318
Dd	121	vshnp1111tpqkvkryyeslwmkssgqpytfid1gml1getl1hnrmt1lslkek	180
QY	319	VNTACCPLEPLFCJLHVKPDVSELNPAWVEFSPYEIGMAKGTGMADPLDGSKFMGTW	378
Dd	181	vntacgplp1f1c1hvpkpdvselmfadwefspyeigmakgyltmapdl1gskfimgtw	240
QY	379	KKYEENPLHFLMGVWSAFSLIFNRVLGVSQSGOSGSGTMEEBELNITTKHIVNSDSSD	438
Dd	241	kkyeenplhflmgvwsafsl1fnrvlvgvsqsgsgtmeee1en1tkh1vnsdssd	300
QY	439	DESHRPKTEHEDDAGSDYQSDONQASWTHRMALVYSSALFNTRBEGAQVHNFMGLNL	498
Dd	301	deshepktehedagdsdyqsdnqaswlhrmaltvssdalfntrregagkvhfm1glnl	360
QY	499	NTSYLSLPSLSPAFODSDFDDELDAAVADPEFERITEPLDVKSCKLHVYDSGLTFNLPY	558
Dd	361	ntsyplsplsfaqdsfdddeldaavadopdeferyepldvkscklhvdydsgl1fnlpy	420
QY	559	PLILRPOGVLDLIISFDESAPRSDSSPFPEKELLAEKWAAMKMLPPEKIDPYVFDREGLK	618
Dd	421	plilrpqgvdl1isfdesarpsdpspfkell1aekwamkmk1pfdk1dpyvfdreglk	480
QY	619	BCYVVRKPNPMEMDCPPIIHFLVLANINFRKYKAPGVPREEKEKELADDDIDDDPSPF	678
Dd	481	bcyvrkpnpmemdcpp1ihflvlaninfrkykagvpreeekeladddidddpspf	540
QY	679	STFNFQYNOAQFKRLLDHMLHNTLNNTIDVIEKAUVESIERYKORPSCSYLSNVEARF	738
Dd	541	stfnfqyngqgfkrllhdmhntlnn1ndviekauvesierytrqprscsvlsnvearrf	600
QY	739	FNKEPLSKPKA 749	
Dd	601	fnkef1skpka 611	

RESULT 9

ID AAY51557 standard; Protein; 913 AA

...
AC AAY51557;

DT	18-MAY-2000	(first entry)
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Human PLAZ protein

AA PLA2: phospholipase A2: phosphatide 2-acyl hydrolase: human: therapy: KW

XX arachnoidic acid; lysophospholipid; Alzheimer's disease.

US Homo sapiens.
XX

PN 056025178-A.
XY

PD 15-FEB-2000.

PF 28-MAR-1997; 97US-0827208.

PR 29-MAR-1996; 96US-0014608

PA (ELIL) LILLY & CO ELI.
 XX Sharp JD, Strifler BA, Cholu XC, Kramer RM, Pickard RT;
 PI
 XX WPI: 2000-181816/16.
 DR N-PSDB: AA288756, AA288757.
 XX
 XX An isolated amino acid having phospholipase (PLA2) activity is useful
 PT in assays to identify inhibitors having a therapeutic benefit, such as
 PT inhibiting the central role of PLA2 in the inflammatory component of
 PT Alzheimer's disease -
 PS Claim 1: Column 53-58; 32pp: English.
 XX
 XX This invention describes a novel human phospholipase A2 (PLA2) protein
 CC (I) and its encoding nucleic acid. The amino acid (I) releases
 CC arachidonic acid in specific tissues characterized by unique membrane
 CC phospholipids, by generating lysophospholipid species which are
 CC deleterious to membrane integrity or by remodeling of unsaturated species
 CC of membrane phospholipids through deacylation/reacylation mechanisms. The
 CC amino acid is useful in assays to identify inhibitors having a
 CC therapeutic benefit, such as inhibiting the central role of PLA2 in the
 CC inflammatory component of Alzheimer's disease. The amino acid (I) allows
 CC sensitive and rapid screening and identification of inhibitors of
 CC phospholipase A2. This sequence represents the human PLA2 protein (also
 CC known as phosphatide 2-acyl hydrolase).
 XX
 XX Sequence 913 AA:
 SQ
 Query Match 18.4%; Score 724; DB 21; Length 913;
 Best Local Similarity 24.8%; Pred. NO. 1.3e-58;
 Matches 208; Conservative 152; Mismatches 268; Indels 210; Gaps 26;
 QY 21 TVVVARATVVTGAGCDMDTPDVELEFISTPDSRKTRFNFNDINVMETPEFLID 80
 DB 145 TVVIVAHIPs---kdlvtpsdcytlwlpacshrlqrltvkssssvwmgsffirh 201
 QY 81 PNOENVLETITLDANYVM-DELTGATFTVSSMKVGE-----KKEVPF--- 122
 DB 202 rqlkhvmeikvtdgdlvtgddpvlsvlfdagtlrgeffsfslspgqegrlvefirg 261
 QY 123 -----TFNOV-----TEMYL----- 132
 DB 262 sladrgewlvsngvlvarelsclhwgleetgdkasehrqlvlpvscegpqeaasygt 321
 QY 133 -----FMSLEVSCSPD----- 143
 DB 322 ftfhpcwgeglslrlqdaeeq[kap]salpsggvtrvlfrtqgeplmrvelkkeag 381
 QY 144 ----LRFSMALDDEKTFRQQRKEHRESMKRLGPKNSEGLHSARDVPVAAILGSGGCF 199
 DB 382 relavrlgfgpaeeagafstrrkqvaalrqal---qldgdlgeelapvalmatrg91 438
 QY 200 RAVGFSGVKALYESGILDCATYVAGLSGSTWYMSLTXSHDPFEK---GPEEINEELM 256
 DB 439 rambtelyglaglkelyldlcvsyitgaagstawaanlyedpewqkdlagptel---lk 495
 QY 257 KVVNSHPFLLLLPQVKRVESIMKKRSKSGOPFTFDIGMILIGELILINRMT--TISL 315
 DB 496 tcytknkilvlpesqldqyrgelaearlgypscfnlwa-llneallndeprdhkslsg 554
 QY 316 KERVNTAQCLPLFLTCILHYK-PDVSELMFADWVEFSPEYIGNAKYGTFWAPDLFGSKFPM 374
 DB 555 relahngqrpilayalnckgslttfegwcefslyvgvfpkyafipelsifseffm 614
 QY 375 GTVVVKYKEENPLPHFLMGWGSAPSLIFNVVLGVSGSQSGSTMEEL-----ENITTH 428
 DB 615 g9lmkrlrlepsticflgslsnyla-----anldgelyasepsqfdwtrw 658
 QY 428 IYNSNDSDDSD---ESHWPKGTEENEDAGSDYQSDNQASWIRHIMTALVSDSALFNTTRG 484
 DB 659 vrnqanldkeqypllkleepstacgrla--effld-----lltwrp 697

QY 485 RAGVHNFMGLINTSYPLSPDSFATQDSFDDDELAAVADPDEFRIYEPLDVNSKK 544
 DB 698 laqathnflrghfhkdyfghp--hfetwkatllgl-----pqg-----lpsaph 742
 QY 545 IHVVDGSLTENLPPYLILRPORGVDLIISPDFSARPSOSSPPEFKLLAEKAKNNKLPE 604
 DB 743 lcldvgyllnscclpllpqtrvdqllslldynlga-----fqqllqllgrfcqegipf 797
 QY 605 PKIDYVDRBGLKSCYEFK-PKNPDMEKDCPTIHFVLININPKRYKAPGVPRTEDEK 663
 DB 798 plpspspeqlprrchctsfqtcp-----gapavlhfrpvsosltreysapgy-ritpca 852
 QY 664 EIADDPIEDDPESPSTENFQYPNQAFKRLHDMHFNLTNINIDVKEAMVESIEYRQ 721
 DB 853 aagevnl-ssdsphyckvtysgedvckllhltynvcmnqegllaalrqaqvrrg 909
 RESULT 10
 ID AAB74635 standard; Protein; 913 AA.
 XX AAB74635;
 AC AAB74635;
 XX 23-MAY-2001 (first entry)
 DT
 XX Phospholipase A2 (PLA2) protein sequence SEQ ID NO:3.
 DE
 XX Phospholipase A2; PLA2; antiinflammatory; inflammatory condition;
 KM Rheumatoid arthritis; psoriasis; asthma; cytosolic PLA2; cPLA2.
 KW
 OS Homo sapiens.
 XX US6197569-B1.
 PN 06-MAR-2001.
 PD
 XX 07-FEB-2000; 2000US-0500358.
 PF
 XX 29-MAR-1996; 96US-0014608.
 PR 19-MAR-1997; 97US-0041264.
 PR 28-MAR-1997; 97US-0827208.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX Cholu XC, Kramer RM, Pickard RT, Sharp JD, Strifler BA;
 PI
 XX WPI: 2001-256372/26.
 DR N-PSDB: AAF74998, AAF74999.
 XX
 XX Novel nucleic acid molecules encoding phospholipase A2 enzyme, useful
 PT in screening assays for identifying compounds that inhibit or block
 PT phospholipase A2 enzyme activity -
 PS Claim 1: Column 53-58; 32pp: English.
 XX
 XX The present invention describes an isolated polynucleotide (I),
 CC comprising a 3085 base pair phospholipase A2 (PLA2) sequence (given in
 CC AAF74999), encoding a 913 residue phospholipase A2 protein sequence
 CC (given in AAB74635), or a nucleotide sequence which hybridizes under
 CC stringent conditions to the above mentioned nucleotide sequence. Also
 CC described are: (1) an isolated polynucleotide (II) comprising an 8517
 CC base pair sequence, given in AAF74998; (2) an expression vector (III)
 CC comprising (I) and an expression control sequence; (3) a host cell
 CC transformed with (III); (4) an expression vector (IV) comprising (II)
 CC operably linked to an expression control sequence; and (5) a host cell
 CC transformed with (IV). (I) is useful for screening compounds which
 CC inhibit or block cytosolic PLA2 (cPLA2) enzyme activity. The host cells
 CC transformed or transfected with cPLA2 enzymes in large
 CC quantities which are useful in screening assays for discovering agents
 CC that inhibit PLA2. The inhibitors identified are useful for treating
 CC inflammatory conditions such as rheumatoid arthritis, psoriasis, or
 CC asthma. (I) is also useful in the detection of mutant genomic DNA which

OY 679 STNFOIPNOAFKRLDLMHFTLNNDIVIKEMVESIEYRRQ 721
 Db 559 hycKvtygsedvdklhlthynvcnqegllleaIrgvqrrr 601

RESULT 13

AAW75132
 ID AAW75132 standard; Protein; 483 AA.

AC AAW75132;

DT 28-JAN-1999 (first entry)

DE Human secreted protein encoded by gene 11 clone HCEMF40.

XX Human: secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 29 /label= unknown

FT Misc-difference 483 /label= unknown

XX W09839446-A2.

PD 11-SEP-1998.

XX 06-MAR-1998; 98MO-US04492.

XX 07-MAR-1997; 97US-0038621.

XX 07-MAR-1997; 97US-0040161.

XX 07-MAR-1997; 97US-0040162.

XX 07-MAR-1997; 97US-0040163.

XX 07-MAR-1997; 97US-0040334.

XX 07-MAR-1997; 97US-0040336.

XX 07-MAR-1997; 97US-0040626.

XX 11-APR-1997; 97US-0043311.

XX 11-APR-1997; 97US-0043312.

XX 11-APR-1997; 97US-0043313.

XX 11-APR-1997; 97US-0043314.

XX 11-APR-1997; 97US-0043315.

XX 11-APR-1997; 97US-0043568.

XX 11-APR-1997; 97US-0043569.

XX 11-APR-1997; 97US-0043576.

XX 11-APR-1997; 97US-0043578.

XX 11-APR-1997; 97US-0043580.

XX 11-APR-1997; 97US-0043586.

XX 11-APR-1997; 97US-0043670.

XX 11-APR-1997; 97US-0043671.

XX 11-APR-1997; 97US-0043672.

XX 11-APR-1997; 97US-0043674.

XX 23-MAY-1997; 97US-0047492.

XX 23-MAY-1997; 97US-0047500.

XX 23-MAY-1997; 97US-0047501.

XX 23-MAY-1997; 97US-0047502.

XX 23-MAY-1997; 97US-0047503.

XX 23-MAY-1997; 97US-0047504.

XX 23-MAY-1997; 97US-0047581.

XX 23-MAY-1997; 97US-0047582.

XX 23-MAY-1997; 97US-0047583.

XX 23-MAY-1997; 97US-0047584.

XX 23-MAY-1997; 97US-0047585.

XX 23-MAY-1997; 97US-0047586.

PR 23-MAY-1997; 97US-0047587.
 PR 23-MAY-1997; 97US-0047588.
 PR 23-MAY-1997; 97US-0047589.
 PR 23-MAY-1997; 97US-0047590.
 PR 23-MAY-1997; 97US-0047592.
 PR 23-MAY-1997; 97US-0047593.
 PR 23-MAY-1997; 97US-0047594.
 PR 23-MAY-1997; 97US-0047595.
 PR 23-MAY-1997; 97US-0047596.
 PR 23-MAY-1997; 97US-0047597.
 PR 23-MAY-1997; 97US-0047598.
 PR 23-MAY-1997; 97US-0047599.
 PR 23-MAY-1997; 97US-0047600.
 PR 23-MAY-1997; 97US-0047601.
 PR 23-MAY-1997; 97US-0047612.
 PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047632.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048974.
 PR 22-AUG-1997; 97US-005630.
 PR 22-AUG-1997; 97US-005631.
 PR 22-AUG-1997; 97US-005632.
 PR 22-AUG-1997; 97US-005633.
 PR 22-AUG-1997; 97US-005636.
 PR 22-AUG-1997; 97US-005637.
 PR 22-AUG-1997; 97US-005662.
 PR 22-AUG-1997; 97US-005664.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057651.
 PR 05-SEP-1997; 97US-0057761.

(HUMA-) HUMAN GENOME SCI INC.
 PA Bednarik DP, Brewer LA, Carter KC, Duan R, Edner R, Endress GA;
 XX Feng P, Ferris AM, Fischer CL, Graves KA, Greene JM, Hu JS;
 PI Kraw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Kiben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX MPI; 1996-609887/51.
 DR N-PSDB; AAV34229.

New isolated human genes and the secreted polypeptides they encode
 PT : useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders

[illegible]

